

937

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTCCTCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTCGCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCCTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAE LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHVRV
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPEKRRISLMFQDYALFPHMSALENAFLGLKMQKMPKAEERLAMAALAEVG					
g593	NGENITCMPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGPETLVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQT PAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDDQGM	ECRVLSRTCLPESF	SLSVLHPEHGILWL	NLDM-RHAGAVSGKDTV		
	: : :	: : :	: :	: : : :		
g593	RHIPQNAVCLDNHGT	ECRLLSLVRLPDSLR	LSAVHPEHGELTLNL	TVGQHTDGISGNGTV		
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:: :					
g593	RIRVDEGRIVRFRX					
	310					

a593.seq

```
1 ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51 CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATATCT GCCGTTTTGG
101 GCGCGTTCGGG CTGCGGCAAA TCCACCTCTG TGAATATGAT TCGCGGCATC
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AATGGGGAGT ACATTACCCG
201 TATGCGCCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTTCCCA TATAGTGTCA CTGGAAAAATG CGGCATTCCG TTTGAAAAAT
301 CAAAAAATCG GCAAAAGCCG AGCCGAAAGC CTGCCATTGG CGGCATTGCG
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAN AAACTTTCCG
401 GAGGCGAAAA GCAACGGTTG GCATCTGGCG GCCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTTGGACGA ATCGTTTTCC AGTTTGACA CGCATTTGCG
501 CGACCGGTCG CGCCGCATGA CTCCGCAAGC TATCCGCAAG GCGGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCCGAAG AGGCCTGAC GCGCGCAGC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGGTT CAACCGCCTG CCGGCGTGCA GGTCGCCCAT CTGATGGGGC
701 TGCCCAATAC CGACGATGAC CGGCATATTC GCGAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTACAG CTGTCCGTCC TCCATCCGGA ACACGGACAT CTGTGGCTGA
851 ACCTTCGATG GCGGCACGCG GGTGAAATAT CGGGAACATG TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCGCTGA
```

```
a593.pep
  1  MLELNLGCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPV EKRIISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI SQTGTPETLV QT PAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DHGMECRLV SRCCLPESES LSVLHPEHGI LWNLNDMPHA GEISGNDTVR
301 IQIDREIVR FR*
```

	10	20	30	40	50	60
m593.pep	MLELNGLCKRFGNKTVADNICLTVGRGKILAVLGRSGCGKSTLLNI	AGIVR	PDGGEIWL			
a593	MLELNGLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNM	TAAGIVR	PDGGEIWL			
	10	20	30	40	50	60
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENA	AFGLKMQKMPKAE	AERLAMA	ALAEVG		
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENA	AFGLKMQKMPKAE	AESLAMA	ALAEVG		
	70	80	90	100	110	120
m593.pep	LENEAHRKPEKLSGGGEKQRLALARALVVRPS	LLLLDES	FSSLD	THLRGT	LR	RM
a593	LENEAHRKPKKLSGGGEKQRLALARALVVRPS	LLLLDES	FSSLD	THLRD	RL	RM
	130	140	150	160	170	180
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI	LQYGT	PETLVKTP	SCVQVAR	LMGLP	NTDD
a593	GGIPAVLVTHSPEEACTTADEIAVMHKGRI	LQYGT	PETLVKTP	SCVQVAR	LMGLP	NTDD
	190	200	210	220	230	240

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```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  GGIPAVLVTHSPEEACTAADEIAVMHEGKIQCCTPETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240
      250      260      270      280      290      300
m593.pep RHIPQHAVRFDQDGMCECVLSRTCLPESFSLSVLHPEHGILWNLDMRHAGAVSGKDTVR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  RHIPQHAVRFDQDGMCECVLSRTCLPESFSLSVLHPEHGILWNLDMPHAGEISGNDTVR
      250      260      270      280      290      300
      310
m593.pep IHIEEREIVRFRX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTTT agcatactcc ggctgctggt ccgcacgga attgggatcg
101 gtaagttcgc cgttcaggcc ttccaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcgggt tgccttgcca ctccgcggtc agcagctgac
201 ccgcttcgat ttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctTTTTTCCG aagggaAAAA actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccggtggt gatttcttga ttatccatta ttcagtcgtc ctaatatTTT
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHFNRFPALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGGCCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCGCGCG CGCAGGTGCG GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTAAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHFNRFPALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKD	VRLNRTGLVFSILRL	LLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP			
g594	MGADTDGDKD	VRLNRTGLVFSILRL	LLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDG	STGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV				
g594	LGGQQLTRFDFTDIHLDG	STGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV				
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTCAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVE SILRLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKD	VRLNRTGLVFSILRL	LLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP			
a594	MGADTDGDKD	VRLNRTGLVFSILRL	LLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDG	STGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV				
a594	LGGQQLTRFDFTDIHLDG	STGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV				
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

```

151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgtgat ggtggtggac gaacgcgaaa atacgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaat tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttggaaa aactgcccc accgctcgcc
451 gactataaaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgatcgc gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttccac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggaacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtt gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa

942

1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggcctt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCACTAT CGCCGTC AAC
 151 GACAATGCCT GCGAACCAGT GGAAGTACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACGCG CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGCG GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGATTGGC
 801 GTTTCCTCCG GCGAAGGTGG TCGGCGGCGC GTCCGAATG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGCTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATT
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
 51 DNACEEMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIAVN	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	130 140 150 160 170 180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE
g595	NPRGKLVVAD SGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAE L FSELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595.pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FET YDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FET YDKLS
	310 320 330 340 350 360
m595.pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAFINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT CGCAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCGA AGCCGTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGTG ATTGAAGAAG
851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSI AVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPGLS

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944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

```

      10      20      30      40      50      60
m595.pep MRKFNLTA LSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
a595      MRKFNLTA LSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT
      10      20      30      40      50      60

      70      80      90     100     110     120
m595.pep VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
a595      VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
      70      80      90     100     110     120

      130     140     150     160     170     180
m595.pep NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
a595      NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
      130     140     150     160     170     180

      190     200     210     220     230     240
m595.pep KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
a595      KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
      190     200     210     220     230     240

      250     260     270     280     290     300
m595.pep DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
a595      DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
      250     260     270     280     290     300

      310     320     330     340     350     360
m595.pep LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG
a595      LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG
      310     320     330     340     350     360

      370     380     389
m595.pep EADRKALQASINALAEDLAQLRGILGLKX
a595      EADRKALQASINALAEDLAQLRGILGLKX
      370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcgggtgga
51 atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggttaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat ttggaactc
151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcgttt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

```

451   ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgccggcggg
501   cgcgattgtc ggcacatcgc gccgaacgc cgcgggttaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgc tgaaaatgag cttgattgac caaagccgcg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgcc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcggccgt ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgttggg atttgccggc agcgtgatgg tgatttcgca
951   cgaccgtggg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgc caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKV NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 ROAKPKARLA RFEEMSNYEY QKRNETQEIF IPVAERLNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSDDQSKIA RQLSGGERGR LHLAKTLGG GNVLLLEDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTC CCTTCTTTC TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGTATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAGCG GTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTGTC
651 GGTAAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTC
951 CGTTGCCGAG CGTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GGTCAAGTTG AAATCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGTCA ATTGTCTGGC
1351 GCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

Homology with a predicted ORF from *N. gonorrhoeae*

	160	170	180	190	200	210
m596.pep	LP EWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTV					
g596						
				MLLDEPTNHLDAESVEWLEQFLVRFPGTV		
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQE					
g596	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQE					
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
g596	LEWVRQNAKGRQAKFKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS					
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLFSFKVPAGAIVGIIGPNGAGKSTLFKFMISGKEQPDSGEVKIGQTVKMSLID					
g596	FGDKVLIDGLFSFKVPAGAIVGIIGPNGAGKSTLFKFMIA GKEQPDSGEVKIGQTVKMSLID					
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR					
g596	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR					
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	DEPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
g596	LHLAKTLLGGGNVLLLD	DEPSNDLDVETLRALED	ALLEFAGSVMVISHDRWFLDRIATHIL			
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGNVQEY	EADKKRRLGEEGAKPKRIKYKPVTRX			
g596	ACEGDSKWVFFDGNVQEY	EADKKRRLGEEGAKPKRIKYKPVTRX			
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTC CTTTCTTTTC TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGAA GCGATTATTG
401 CGCGCGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCGCAGCGGC TGCGCTGCC GGAATGGGAT GCCAAATCG ATAATTGTC
501 CGCGCGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGAGCAATT TCTCGTGC GC TCCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGGAAGAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTC AAGCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCAGGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVPPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEP LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAE WILELDRGHG IPWKNYSWSW
251 LEQKEKRLEN EAKSEARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV QFELPARQY LGRENFKGSD QSKITGQLSG
451 GERGRHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEY EADKKRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQRTTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQRTTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDPEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLLDPEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEYADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGAKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq
 1 ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
 51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
 101 TTGCTTCCGT CAACCGCAA CAGCGGAGG CTTGGGACAA ATTCCAAAA

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTC CGTTTCGTAT CGGGGAAC TA AAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCCGAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TTCaggAtgc ggAagcaaAA agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGCGCAG CAGAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggC GATGTTTGA AAGCGGTGT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCg gAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGCT TTGAGCGAAA TTTCCGCCG CAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCAG AGCGGGTCG TGCCGGACGG
1101 GGAAGAGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

```

g597.pep
1 MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVAFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQNLN LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAQA QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISYIAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

```

m597.seq
1 ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAAGTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCTGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCGGGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAAACAGC
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAGAAAAAT TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCCG AGACAGAATG CCAAATCGC
501 CAAAGATGCC CGAAAACTGC TGGAAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGGTGAA GCCAGACTGG CGGCAGCCGA
651 AAAGGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTGCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAAGTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTGC ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATAA CGTTATCAAG GTCAGGTATT GAACCCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

```

m597.pep
1 MLLHVSNSLK QLQEEIRQE RIRQARGNLA SVNRRQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV KLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAAEQTESR QNAKIAKDA RKLLEQKQNE QQLNKLNLN EKKKAHRIQ
201 DAEAKRLAE ARLAAAEKAR KEAAQKAEK RRAEMSNLTA EDNRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGVNLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRLKT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQQKINNELLARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQQKINNELLARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELGYGKVVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELGYGKVVVDHGENYISIIYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGA AAAA CAGCAGAAG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTGAG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCCTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCAGCAGC TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACCT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGCG GATGTTTGGA AAGGCGGTGT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGGTCGG CAAGGGTTAT
1051 ATGCTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFKQ
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQQQ VLNPFSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

a597.pep	10	20	30	40	50	60
	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFKQLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFKQLNTELNLRLKT					
	10	20	30	40	50	
a597.pep	70	80	90	100	110	120
	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
a597.pep	130	140	150	160	170	180
	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
a597.pep	190	200	210	220	230	240
	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
a597.pep	250	260	270	280	290	300
	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
a597.pep	310	320	330	340	350	360
	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
a597.pep	370	380	390			
	SGSLPDGEEGLYLQIRYQQQVLNPFSSWIRX					
m597	SGSLPDGEEGLYLQIRYQQQVLNPFSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCCG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCGCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCGGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcggtca
551 tgaGCCGCGC CGCACgcgtg attatggaaa gttgGGTGcG cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDGGWTAA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGLTVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDGGWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

```

              10      20      30      40      50      60
m601.pep      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
              |||
g601           MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
              10      20      30      40      50      60

              70      80      90     100     110     120
m601.pep      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
```

953

g601	TIRAYGALKMGLISDVSEAAARARPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG	70	80	90	100	110	120
m601.pep	KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT	130	140	150	160	170	180
g601	KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT	130	140	150	160	170	
m601.pep	ATKAVMSRSARVMMEGWVRVPEDCFX	190	200				
g601	AAKAVMSRSARVIMESWVRVPDDCFX	180	190	200			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GCGCGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGTTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE	10	20	30	40	50	60
a601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE	10	20	30	40	50	60
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG	70	80	90	100	110	120
a601	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG	70	80	90	100	110	120
m601.pep	KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT	130	140	150	160	170	180
a601	KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT	130	140	150	160	170	180
m601.pep	ATKAVMSRSARVMMEGWVRVPEDCFX	190	200				
a601	ATKAVMSRSARVMMEGWVRVPEDCFX	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA TgcgagattA TATCACTTGC TTTtgccgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGO INRHQASNR GLCSFGGFG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLAA
101 CLQMRDYITC FWRHL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIIHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
g602	MLLHQCDKARHMRPFLGGOINRHQASNRGLCSFGGFGQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNIIHVIEMCAWYGVSAGEYTVN---LQMRDYITRFQXLHX					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLAAACLQMRDYITCFWRHLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIIHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRPLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQXLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQXLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCAC AACTACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTC TACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCG AACTGCCAG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCGGTGCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCGCCC GCTACGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGTAATAGGG TACACGTTGC GGCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGC CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTGACGCAC TCGTGTTCAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT TTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAA CGCTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTPP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPEAYTY AVPRELRKKY AFRRYGFHGT GMYVAPPEA RILGKPLEDI
251 RMIIAHLNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPN DCRTL EIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYGNISGIISP TDSSPAVLV PTNEELMIAC DTABLAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTGACGACA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGCGGCC GTTATCGACC GAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

1	LSSRRRRGRNN	DRKCGIRFAQ	RGRCLKHLAPD	VCXFSDDP TL	KKQPQOTTRRN
51	IMSDQLILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGERLTT	PEAVITFNKD
101	GNKRQVPLSG	RNCHACAVGM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIPLAP	LHNPNANISGI	LAAQEHFPGL	PNVGVMDS TF
201	HOTMPERAYT	YAVPRELRKK	YAFRYGFHGG	TSMRYVAPEA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSVDTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTLEIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASNAVCGG	GVDALVFTGG	IGNSRNRIRA	KTVSYLD FLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAE LAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

m603/g603

		10	20	30	40	50	60
m603.pep		LSSRRRGRNNDKRCGIRFAQGRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
		:: ::		::	:		
g603		MDSRLRG-NDARKYGIRFAQGRGLKHTPPNAHPFSDGPAKKQPQTTRRNIMSDQLILVL					
		10	20	30	40	50	
		70	80	90	100	110	120
m603.pep		NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKQVPLSGRNCHAGAVGM					
g603		NCVSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFNKDGNGKQVPLSGRNCHAGAVGM					
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603.pep		LLNELEKHGLHDRIKAIGHRIAHHGGEKYSESVLIDQAVMDELNACIPLAPLHPNPNANISGI					
g603		LLNELEKHGLHDRIKAIGRRIAHHGGEKYHESVLIDQDVLDELKACIPFAPLHPNPNANISGI					
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603.pep		LAAQEHFPGLPNVGVMDSFSHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA					

957

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g603      LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISSELSNDCRTLEIAADEGHEGARLALLEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISSELPNDCRTLEIAADEGREGARLALLEVMTCLRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1  CTGTCCTCGC GTAGCGGGG ACGGAATAAC GATAGAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCGGTC TGAACACAC TCCGCCAAC GCCCATCCTT
101 TTTGAGACGA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAAGT CACGACCGCA
401 TTCAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCCAATGTCT GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCGG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGG TTTCCACGG ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGGC AAATCCGTCTG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCTCTGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAAGT GATGATTGCC TGCGACACTG CCGAAGTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1  LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHN PANISGI LAAQEHFPGL PNVGVMDTSF

```

958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVMTYRLAK YIASMAVCGG GVDALVFTGG IGENSRNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQRGRKLHAPDVCXFSDPTLKKQPQTTRRNIMSDQLILVL					
a603						
	10	20	30	40	50	60
m603.pep	70	80	90	100	110	120
a603	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKQVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
m603.pep	130	140	150	160	170	180
a603	LLNELEKHGLHDRIKAIGHRIAHGGEKYESVLIQAVMDELNACIPLAPLHNPNANISGI					
	130	140	150	160	170	180
m603.pep	190	200	210	220	230	240
a603	LAAQEHFPGPLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSRMRYVAPEA					
	190	200	210	220	230	240
m603.pep	250	260	270	280	290	300
a603	ARILGKPLEDIRMIIAHLGNASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
m603.pep	310	320	330	340	350	360
a603	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK					
	310	320	330	340	350	360
m603.pep	370	380	390	400	410	420
a603	YIASMAVCGCGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
m603.pep	430	440	450			
a603	PTDSSPAVLVPTNEELMIACDTAELAGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:
 g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT CGAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GGCGTGGCG CGCGGCGGC GCCTTCGGAT

g604 . pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FORAICADGF
101 KFFQRGGIV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDOIAGWEHT AFAVGWI*

```

m604.seq

m604 . pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVQ FAHAQGAYQQ
51 IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFORTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDOIAGWE HTAFAVGWI

```

Homology with a predicted ORF from *N. gonorrhoeae*

m604/q604

```

                                10      20      30      40      50      60
m604 .pep    MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVQFAHAQGAYQQIDVGGVHGFA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g604          MPEAHFFTRSAACGKVDQRTEHGGG--DGDGRDAHHSVVQFAHAQGAYRQIDVGGVYGF
              10      20      30      40      50

                                70      80      90      100     110     120
m604 .pep    TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGI VDVVLQLFA
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g604          AGGGVIGGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGI VDVVLQLFA
              60      70      80      90      100     110

                                130     140     150     160     169
m604 .pep    CVAQVGGIQENGRNARVDERG FQTAYIRHINFIDQIAGWEHTAFAVGWI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g604          RVAQVGGVQENGRNARVDERG FQTTYIRHINFVDQIAGWEHTAFAVGWIX
              120     130     140     150     160

```

a604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGCACGGCG GCGGCGGTGC CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGGCG GTACCAGCAA
151 ATCGATGTGC GCGGCATTCA CGGTTTGGCC ACTGGAGGCG GTGTAATCGG

960

```

201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAGGAA AACGGTCGGA
401 ATGCCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

-- This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1 MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGIHFQA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFVAGWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

```

          10      20      30      40      50      60
m604.pep MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGF
          |||||:|||||:|||||:|||||:|||||:|||||
a604      MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHF
          10      20      30      40      50      60

          70      80      90      100     110     120
m604.pep TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA
          |||||:|||||:|||||:|||||:|||||:|||||
a604      TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA
          70      80      90      100     110     120

          130     140     150     160     169
m604.pep CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWI
          |||||:|||||:|||||:|||||:|||||
a604      RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWIKFDLYFGCRE
          130     140     150     160     170     180

a604      RYAVELKIACFQNCVHLHRYMGNNGFADVFLPDFDCADAVX
          190     200     210     220

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgcca agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCGCCTCC GGCTAaccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCGTCCTT TAAAGGCGTG GCGGAACTCG ATTTCCGGCA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCTAATA CGCcgcCAAC GCAGGCAAA CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAAGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GCGGACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAA CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

```

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDFTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIIIEGFF
251 GQEIHNHTYIN LARMNMFLHN VNYNKFHIEL GDTLTNPKLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLCHKHNDT DIQFIDASGF FKKETNNNV L TEEHIAEIVK LPADKADVPH
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGAAG
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACGCG ATTTCCGGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLAAVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQSEINHTTYN LARMNMFLHN VYNQFHIEL GDTLTNPKLK DSKPFDIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVPH
 451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.pep	10	20	30	40	50	60
	MMTEMQRAQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	10	20	30	40	50	60
	MMTEMQRAQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
m605.pep	70	80	90	100	110	120
	YAAMPDSIITPEIKDDAVKVKGFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	70	80	90	100	110	120
	YAAMPDSIITPEIKDDAVKVKGFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
m605.pep	130	140	150	160	170	180
	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGNFENHHIDLFGDAY					
g605	130	140	150	160	170	180
	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEELDFGNFEDHRIDLFGDAY					
m605.pep	190	200	210	220	230	240
	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
g605	190	200	210	220	230	240
	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
m605.pep	250	260	270	280	290	300
	DEHIEEGFFGQSEINHTTYNLARMNMFLHNVNQFHIELGDTLTNPKLKDSKPFDIVS					
g605	250	260	270	280	290	300
	DEHIEEGFFGQSEINHTTYNLARMNMFLHNVNKFIELGDTLTNPKLKDSKPFDAVVS					
m605.pep	310	320	330	340	350	360
	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI					
g605	310	320	330	340	350	360
	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI					
m605.pep	370	380	390	400	410	420
	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNIVLSKHKDNTDIQFIDASGF					
g605	370	380	390	400	410	420
	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGCIAVNIVLSKHKDNTDIQFIDASGF					
m605.pep	430	440	450	460	470	480
	FKKETNNNVLEEHIAEIVKLFADKADVPHIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLEEHIAEIVKLFADKADVPHIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	QLHRQIWKI	ADVEVRG	AVDGVDF	KQYVLGT	LFYRFISENFTDYM
a605	MMTEIQQR	QLHRQIWKI	ADVEVRG	AVDGVDF	KQYVLGT	LFYRFISENFTDYM
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	IIITFEIK	DDAVKVG	YFYIPG	QLFCNIA	AEAHQNEELNTKLKEIFTA
	ESSAS					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

1	ATGTCCAAAT	TTATCGCCAA	ACAATCGGTC	GGTGC GGAAG	TCATCGACAC
51	GCCGcgCACC	GAAGAAGAAG	CCTGGCTTCT	GAACACTGTC	GAAGCCCCAag
101	cgcGGGCAATg	GAATCTGAAA	AGCGCAGAAg	TCGCCATCTA	CCACTCCCC
151	GAACCCAATG	CCTTTGGCCAC	GGCGCGCATCG	AGAAACAGCT	CCCTGATCGC
201	CGTCAGCacc	ggtttctctcg	acctatgaC	GCGCGACgaa	gtggaagcgcc
251	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGCATG	GATTACGCTG
301	ACGCTGatTC	AAGGCGTGGT	CAATACCTTT	GTCTGTTCC	TGTCGCGCAT
351	TATTGGCCAAC	CTGATTGCCG	GAACAACAGA	CGCGACGCCAG	TCCCAGGGAA
401	CTTATTTCCT	AGTCAGCATG	GATTTCCAAA	TCCTGTTCCGG	CTTCCTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCGCCCAA	CGCGAATACC	GCGCCGAcgc
501	gggCGcggCA	AAACTGGTCG	GCGCACCGAA	AATGATTTC	GCCCTGCAAA
551	GGCTTAAAGG	CAACCCGGTG	GATTTGCCCG	AAGAAATGAA	CGCAATGGGC
601	ATCGCCGGAG	ATACGCGCGA	CTCCTTGCTC	AGCACCCACC	CTTCGCTGGA
651	CAACCGAATC	GCCCCGCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCC GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIIVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIIVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCGCGCACCC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 GCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AACTGGTCG GCGCGCCGAA AATGATTTC GCGCTGCAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCGA CTCCTGCTC AGCACCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVALHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVNGDMVTLTLIQGVVNTFVVFLSRIIAN
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVNGDMVTLTLIQGVVNTFVVFLSRIIAN
m606.pep	LIARNNDGSQSQGTFFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
a606	LIARNNDGSQSQGTFFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TCGCGGCAAG
151 GAAGATTGGC CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGCGAGGGG
301 ATTTGGTTCG GGCTGATTTT GGGGATTTTC GGCATGATTT TGATGTGGGC
351 GCGGATTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCGC
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGTGGCGCA

```

```

601  GGTTCGCGCG TGGCGACAAT GCGGGTGTTC TGGTTCAGCG CGCTGGCATT
651  GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGAATGACAG
701  CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751  gGcgcgCCCA TCGGGCTGTC TTATTTTGTG GAAgccaGcg cGTTTTTCGTT
801  TATCGTGTTC TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851  AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901  GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951  TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTG GGTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGATCC GGCAGTTTAA AGCATCGCCT CCACCGTCCT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTACCCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

```

g607.pep
1  MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAIT PFRNWLTLSD YVEGTMAYQM LFTSLAMPAA
151 MVHRAHAYHA SSLNRPRLLIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSEFIV LIAPFGEDYV AAQVGGISLS GILYMIPOSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASVTLLFA GLFQPADFTQ CIASYALRGY KVTKVPMPFIH
401 AAAPFWGGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

```

m607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTGTG GATACTGTGA TGGCGGGCGG TCGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GACGAAGTG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGGTGTTC TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAATC
751 GCGGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTAA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCCT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

```

m607.pep
1  MLLDLNRFSF PVFLKEVRLT TTLALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/q607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPFVFLKEVRLLTTLALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLA AVALGS					
	: : : :					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLA AVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNP MIAQLYGAGKTDEVGETGRQG IWFGLFLGVFGMVL MWAAIT					
	: : :					
g607	SAFATVYITFMGIMAALNP MIAQLYGAGKTGEAGETGRQGIWFG LILGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQ YMLFTSLAMPAAMVHRALHAYTS SLNRPRLLIMLV SFAAFVLN					
	:					
g607	PFRNWLTLSDYVEGTMAQ YMLFTSLAMPAAMVHRALHAYAS SLNRPRLLIMLV SFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGG AGCGLATMAVFWFSSALALWIYI AKENFFRPFGLTAK FGKPD					
	:					
g607	VPLNYIFVYGKFGMPALGG AGCGVATMAVFWFSSALALWIYI AKEKFFRPFGLTAK FGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSY FLEASAFSFIVFLIAPFG EDYVAAQQVGISLS GILYMPIQSV					
	:					
g607	WAVFKQIWKIGAPIGLSY FLEASAFSFIVFLIAPFG EDYVAAQQVGISLS GILYMPIQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFS RARYISGVSVLVGWMLA VITVLSVLVFRSP LVSMYNNDPAVL					
	: : :					
g607	GSAGTVRIGFSLGRREFS RARYISGVSVLVSGWLVAVITV LSVLVFRSP LASMYNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFT QCIASYALRGYKVTKVP MFIIHAAAFWGCG LLPGYLLAYRFN					
	: :					
g607	SIASTVLLFAGLFQPADFT QCIASYALRGYKVTKVP MFIIHAAAFWGCG LLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAA IALVWCLELCSREMVR SHKAVX					
	: : :					
g607	MGIYGFWTALIASLTIAA IALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCGT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTGGGCGAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGCAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTC GATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCCT GCGCGCTAC AAAGTTACAA AGGTCCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLT TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVEF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 CGGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQVVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFHI
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCR
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

```
m607.pep      10      20      30      40      50      60
MLLDLNRFSF  PVFLKEVRLT TALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS
|||||
a607          10      20      30      40      50      60
MLLDLNRFSF  PVFLKEVRLT TALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS

m607.pep      70      80      90      100     110     120
SAFATVYITF  MGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVLFGMVLMWAAIT
|||||
a607          70      80      90      100     110     120
SAFATVYITF  MGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVLFGMVLMWAAIT

m607.pep      130     140     150     160     170     180
PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLAHAYTSSLNRPRILMLVSFAAFVLN
|||||
a607          130     140     150     160     170     180
PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLAHAYTSSLNRPRILMLVSFAAFVLN

190      200      210      220      230      240
```

970

```

m607.pep      VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPIQSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADEFTQCIASYALRGYKVTKVPMFHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADEFTQCIASYALRGYKVTKVPMFHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACC CGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa cAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGLDILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACC CGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCGGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```


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501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	::					
g608	MSALLPIINRLILQSPDSRSELTSFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEFGAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	::					
g608	TFRNSAIRKILQGGEFGAGDIRLEGLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGKIQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGKIQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGAAACG GCTTTGCAGA CACCGAAATC ACCTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG
301 CGTTCGCCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep  MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
           10      20      30      40      50      60

           70      80      90      100     110     120
m608.pep  TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608      TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
           70      80      90      100     110     120

           130     140     150     160     170     180
m608.pep  RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608      RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
           130     140     150     160     170     180

           189
m608.pep  LERDIWIDX
a608      LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTG GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCGTCTTT CATTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDAFV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRPHIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTG GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CCCCGTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDAFV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRPHIIDNF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60
g609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRPHIIDNFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

```

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```

g609      RLRFHIIIDNFDLDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |:|:|:|:|:|
g609      HFTREADIIIQX
           130

```

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```

a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AACTCTTGA
51  TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```

a609.pep
1  MVVDRLEILA LDEETLDAFV GNQRSSDIAH HIFHEFRV FV GFFGNVFFIG
51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*

m609/a609 96.9% identity in 131 aa overlap

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FV GFFGNVFFIGAFEQAVELAA
           |||
a609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FV GFFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRHLIIIDFLDFTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           |||
a609      RLRHLIIIDFLDFTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |||
a609      HFAREADIIIQX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```

g610.seq
1  ATGATTGGAG GGCTTATGCA ATTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCGTG ATGCGCGAGC
101 ATATGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTTCT ATTGGAGGGG
151 GCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTGAAG CTCGGTATTC
251 CGATGTTGGC ACTCTTTCCC GTGGTTACGG CAAACAAAC CGGGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG tccgagccTT
351 GCGCGAGAGG TtccCgaac tggggattat gacggatgtc gcgctcgAtc
401 cttatacggT gcacGGTCAG GACGGACTGA CGGACgaaaa cggttaCGTG
451 ATGAatgATg aaacCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGGCGTA
551 TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGGG AAAGGCAGAT AAAAAGACCT
701 ATCAGATGGA TCCTGCAAAT ACCGATGAGG CGCTGCATGA AGTGGCGCTC
751 GATATTACAG AAGGTGCGGA TATGGTGATG GTGAAGCCCG GTTGGCCGTA

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801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
 851 CCTATCAGGT TTCGGGCGAA TATCGGATGT TGCAGGCGGC GGTGCGCAAC
 901 GGTGCGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
 1001 AGATGCTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

m610.pep
 1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
 51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
 101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
 151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KPTYQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAVAN
 301 GWLDGGKVVL ESLLAFLKRA ADGILTYAI EAAKMLKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq
 1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
 51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCGCGCTG ATGCGCGAAC
 101 ACACGCTGAC CGCCGATGAT TTGATTATAT CCGGTGTTCT ATTGGAGGGG
 151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
 201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAGG CTCGGTATTC
 251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
 301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
 351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
 401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
 451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
 501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
 551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
 601 ATTATGCGGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
 651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT
 701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
 751 GACATTGAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTGCCGTA
 801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
 851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
 901 GGTGCGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
 1001 AGATGTTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep
 1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
 51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
 101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
 151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIRES LEDAGHIHTR
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KPTYQMDPAN TDEALHEVAL
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAIAN
 301 GWLDGGKVVL ESLLAFLKRA ADGILTYAI EAAKMLKR*

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREHMLT	ADDLIYPVFVLE	GSAREEDVPSM	
g610	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREHMLT	ADDLIYPVFVLE	GAAREEDVPSM	
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLL	FTAEEAVKLGIP	MLALFPVVTANK	TERAQEAYNPE	GLVPSTVRALR	
g610	PGVKRQSLDRLL	FTAEEAVKLGIP	MLALFPVVTANK	TGRAQEAYNPE	GLVPSTVRALR	
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPGLGIMTDVAL	DPYTVHGQDGL	TDENGYVMNDET	VEVLVKQALCH	AEAGQVVAPSD	
g610	FPGLGIMTDVAL	DPYTVHGQDGL	TDENGYVMNDET	VEVLVKQALCH	AEAGTQVVAPSD	
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLE	DAGHIHTRIMAY	SAKYASAFYGP	FRDAVGSSGNL	KGADKPTYQMD	

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g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCCCGCT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCGGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGCGCAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTCCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGFPRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVV ELLAFKRAG ADGILTYYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

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```

m610.pep  FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
a610      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
           130      140      150      160      170      180

           190      200      210      220      230      240
m610.pep  DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
a610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
a610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
a610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGGCG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 taticctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctga
251 TcgcgGTcta tggtttccCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTCatcga ggaTTTGTa ggcaacCTGA TACTgtcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt TTTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGtc gCTCatgcG TAGCGCGTTA
501 CCATTTCCGC TGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKGR QLAGCRLFGK LSLVFRLLPG LCRGVCVRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGGCG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTCGACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTtAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKGR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
              |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCGG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTGGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF PPFHQGFARHFL
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611 |
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq
1 ATGGGcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51 AGCCTtttgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCgATTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep
1 MGFGGNIKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq
1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTTAAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep
1 MGFGGNIKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAGVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq
1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT .AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttT.AC GGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NTAVACLHIV
 51  GKVFDKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep     MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINTAVACLHIVGKVFDKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep     KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          KCAENVLFEPV AIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep     GHSNX
              ||||
a612          GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgctgcc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  CCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTACAGG CTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCgGA CTCGATTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGCTGCC TGCCTGCCGA AAATCCGTGC CAATTCTGCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  CCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1 MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSA
 51 FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSA					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMFACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
g613	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDRGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTCGCGGA  CTCGGGTTTCG  CGGGAAAATC  TGCCGATTTC  TTCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCGTCC  TGCCTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTCGCC  CGCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCGGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGCGGCGAA  GTTCCGAGCG
501 GCTGTCGGG  CTTTGACAG  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTTGCT  GTTGACGCTT
601 ATTTTACAGG  CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
51  FLPICLMPCE  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSAPAG  SPPWRIFCTA  LLRKVISVSA  KPFAESKPS  SVMRPASFPN
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSDS	RENPPICSAMFLPICLMPCP			
a613	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSDS	RENPPICSAMFLPICLMPCP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPMKIRANSS	DARERRLPSRDSTAMPRMRSP	SSPMSPAPGSPWRIFCTA			
a613	MSAARLPMSACVPMKIRANSS	DARERRLPSRDSTAMPRMRSP	SSPMSPAPGSPWRIFCTA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
a613	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq
 1 AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acggggcaaat
 51 cgaaTATCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGATG ACAACCTGAT
 201 TCAAACCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCTa
 501 tcaAAGcctc ggcgggcgtg ttcCGGCGG CATCctgCtg gcgGgcagcc
 551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
 601 GTGCCGTTCT TCAGCATTTC CGGTTCGAT TTTGTCGAAA TGTTCTGTCG
 651 TGTCCGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
 701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
 751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGGACA TCCGGGGCGG
 951 CGAACAGatn ttGAACGTCC ATTCTaaAAA AGTGCcttTG gacgaATCTg
 1001 tggaTTTATT GTCCCTCGCG CGCGGCACGC ccggttttTC cggcgcgat
 1051 tTggcgaaac tggTcaacga agccccctg tttgccggcc gccgcaacaa
 1101 agtgaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGA CGCCGAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep
 1 MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
 51 TDKSTFFTNA PLDDNLIQTL LNKNVVRVKVT PEEKPSALTA LFYSLLPVLL
 101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDKANKVT FADVAGCDEA
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
 301 GRFDRQVVVP LPDIRGREQX LNVHSHKKVPL DESVDLLSLA RGTPGFSGAD
 351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51 CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGATG ACAACCTAAT
 201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
 251 AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
 301 CTGATTGGCG CATGGTTCTA CTTATGCGT ATGCAGACGG GCGGCGGCGG
 351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
 401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
 451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
 501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
 551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
 601 GTGCCGTTCT TCAGCATTTC AGGTTCGAC TTTGTCGAAA TGTTCTGTCG
 651 TGTCCGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
 701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
 751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
 801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
 851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
 901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGGACA TCCGAGGGCG
 951 CGAACAGATT TTGAACGTCC ATTCTAAAA AGTGCCTTTG GACGAATCTG
 1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
 1051 TTGGCGAAT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
 1101 AGTCAAAGTC GATCAGAGCG ATTGAAGAC GCCAAAGACA AAATCTATAT
 1151 GGGTCCGGA CGCCGAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51  TDKSTFTTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DESVDLLSLA RGTGFGSGAD
351  LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFTTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFTTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG					
	: : : : :					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLLPVLL LIGAWFYFMR MQAGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIAAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAAGEAG VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQR GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGT GFGSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQXNVHSHKVPLDESVDLLSLARGT GFGSGADLAKLVNEAAL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201  TAAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCGAGCGC GCTGGCTGCC CTGTTTACAC GCCTGCTGCC CGTCTGCTG

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984

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGGCGTTTCG ACCGCCAAGT GGTGTGCCCG CTGCCGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTATTT GTCCTCGCG CGCGGCAGCG CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

a614.pep

```

1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGK AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

m614/a614 99.7% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
a614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTLDDKNVRVKVTPEEKPSALAAALFYSLLPVLLLIGAWFYFMRMQTGGGKGK					
a614	PLDDNLIKTLDDKNVRVKVTPEEKPSALAAALFYSLLPVLLLIGAWFYFMRMQTGGGKGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
a614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTLLAKAIAEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
a614	AGSPGTGKTLLAKAIAEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQRGAGLGGGNDEREQLTNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
a614	DEIDAVGRQRGAGLGGGNDEREQLTNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHKKVPLDESVDLLSLARGTGPFGSGADLANLVNEAAL					
a614	GRFDRQVVVPLPDIRGREQILNVHKKVPLDKSVDLLSLARGTGPFGSGADLANLVNEAAL					

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCGGAAa  gcaggCtgaa  gcGGTTgcgC
101  GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151  aggcgcAGGa  ATTTGcgcCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201  cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTcG  TACagcagga
251  aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301  ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351  gAaagggtct  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401  cctcttccca  ttgCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451  gCGACGGcat  cgctgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501  agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGTgggc  GATGCCGAGG
551  CGCAGCGCGT  aatagtctgc  CGTCCGAGT  TTTGCctgAA  TGCTTTTCAA
601  GCCGTTGTGT  CgcCGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCCG
651  AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801  CAACTTCGCC  GAAGAATTTT  TTTCTTCTT  TAAACGAAGC  CTTCATTTC
851  CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGTCTGTTC
901  GTATTCTTTG  CCCGGGTGTC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951  acatgataTT  TtccgtgTTT  CTgTCGaag  cggCtgaAG  GCTTCAGacg
1001  gcatggTtat  TCTTCTTgaT  TTtgaACcg  tgtgcggCGC  GCTTCTTTGG
1051  GGTCGATCAA  CAGCGGCGG  TACACTTCGA  TCGGGTCGCC  GTCGCGCAGC
1101  GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101  LSSFMTVRIR  KSGKRLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151  ATASSICRRR  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201  AVVSAVAAAE  FEFDPsARDV  EFVVDDEDF  GFDFVELCKR  GNRLSGTVHE
251  RGRFEQPNIA  VGQGGAGNFA  EEEFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301  VFFARVAQAD  NHFDCVRHDI  FRVSECGLK  ASDGMVILLD  FERVCGALLW
351  GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1  ATGCGGAAAA  GCGGTTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101  GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151  AGGCGCAGGA  ATTTCCGCC  GCGTGGCGCC  AGCATATCGC  GCCAAACGGC
201  AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTcG  TAGAGCAGGA
251  AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCGGTTTG  GATAAGCTGC
301  TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351  GAAAGGGCTT  CAGACGGCAT  CGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401  CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451  GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501  GGACATAGCC  GACGACGAGG  TTGCGGTGCG  CCGGGTGGCC  GATGCCGAGG
551  CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601  GCCGTTGTGT  CCGCGTTGTC  CGCCGCGGAG  TTTGAATTTG  ATCCGTCCGC
651  AGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

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986

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CAAAAAAGCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTGTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTGCAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAVAEE FEFDPAGNV EFVVDDEDFG GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDFE EEEFFFKXS LPFPQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHD IFRVSVECLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LDRRRNFPPRAA		
g615	MRKRRWRGFGSFEKQXVNA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LDRRRNFPPRAA		
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
g615	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSICR	RCXRTGFVQDIADDEVAVARVA			
g615	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSICR	RCFRARFVQDVADDEVAVAGVA			
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQ	AVVSAAVAEEFEFDPAGNV	EFVVDDEDFG	GFDFVELCKR		
g615	DAEAQAVIVCRAEFCLNVFQ	AVVSAAVAEEFEFDPAGNV	EFVVDDEDFG	GFDFVELCKR		
	190	200	210	220	230	240
m615.pep	GNCLSGTVHERGRFEQPNV	AVGQGGTGDFAEFFFKXS	LPFPQFVEE	PKTRIVACLF		
g615	GNRLSGTVHERGRFEQPNV	AVGQGGTGDFAEFFFKXS	LPFPQFVEE	PKTRIVACLF		
	250	260	270	280	290	300
m615.pep	VFFARVAQADNHFDCVXHD	IFRVSVECLKASDGMVILLD	FERVCGALLW	GRSTAGGTLR		
g615	VFFARVAQADNHFDCVXHD	IFRVSVECLKASDGMVILLD	FERVCGALLW	GRSTAGGTLR		
	310	320	330	340	350	360
m615.pep	CGRRRAAACRLX					
g615	CGRRRAAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GCGCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCAGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTGTTGTCA
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCGGAG TTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCGAG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCCGATCAA CAGCGGGCGG TACACTCGA TCGGTCGCC GTCGCGCAGC
1101 GGCGTGTCTG CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLP A RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDF GFDIFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDFE EEEFFFK*S LFFPRQFVEE BKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*

m615/a615 90.3% identity in 371 aa overlap

10      20      30      40      50      60
m615.pep MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHSIDRRRNFPRAA
||||| || ||||| :||| ||||| :||| :||| :||| ||||| :||| :|||
a615      MRKRRRRGVGSFEEQRIDAAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA
10      20      30      40      50      60

70      80      90      100     110     120
m615.pep SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
|:|:| | |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
70      80      90      100     110     120

130     140     150     160     170     180
m615.pep QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA
130     140     150     160     170     180

190     200     210     220     230     240
m615.pep DAEAQAVIVCRAEFCLNVFQAVVSAAAEFEFDPAGNV EFVVDDEDFGFDVELCKR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNV EFVVDDEDFGFDIFIKLRKG
190     200     210     220     230     240

250     260     270     280     290     300
```

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFKXSLFPFPRQFVEEPKTRIVACLF
a615       GNCLSGTVHERGRLEQPDIAVGQGGTGDFAEFFFKXSLFPFPRQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCVXHDIFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
a615       VFFARVAQADNHFDVCVXHDIFRVSACRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
a615       CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCG TTTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCC TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GcgggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccac CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg Ccggcaaatc gacgatGCCG
501 TCGCCaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gctTCCTGCA CAGCAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgc cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC cgtcatcga agaaacctc
701 gatttctcgc tGTACGAATG cagcAtcgc gaagCACcgt ccgcccgaaga
751 agtggcacia TGcgcgacac tactTGcgcg acgcgGcgGC AAATtCCTGc
801 gcctgtccaa aatctgcCaa aCGTGGctGG ACgAGGAGGC GGCatgAAgc
851 tGGCGcgcaa CCgcttcaGc ctgctTTCCG CATTTGgGTt TGCCGGCGGC
901 atctATtCgc tgctcttcaa AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTtccaA AAAGCAGCAC ACCTTGCCCT GTTTTCGCA CaaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAaAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGCAGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTGCCG CCGCTTCTGC CTGCCGccgc
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEP PANRRCRRQI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSREPY PNSHRTQAA YPNIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPYPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSIGDV LADLTGAALA LFAARSACRP
401 D*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCGCGTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCACT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCC TCCACGACGA ACTCGACATT
301 CCTTGGCGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCAAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

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989

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GGGNGHNLK DIQAKLGTD YVRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QQMTRCRLK
201 FQTACSRFPY PSHDRTOAA YPNRIHPRHR RNPRFPALRM QHRCPLRRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLGDV LADLTGAALA LFTARAACRP
401 D*

m616/g616 86.0% identity in 401 aa overlap

m616.pep      10      20      30      40      50      60
MSNTIKMVVGLG NPGKEYEQTR HNAGFWFLDE LAWKWKASFKEE KKFGEVARAAL PDGD
|||||
g616          10      20      30      40      50      60
MSNTIKMVVGLG NPGKEYEQTR HNAGFWFLDE LAWKWKASFKEE KKFGEVARAAL PDGD

m616.pep      70      80      90      100     110     120
VWLLKPATFMNR SGQAVALAQFY KIKPEEILVVH DELDIPCGRIK FKLGNGGHNLK
|||||
g616          70      80      90      100     110     120
VWLLKPATFMNR SGQAVALAQFY KIKPEEILVVH DELDIPCGRIK FKLGNGGHNLK

m616.pep      130     140     150     160     170     180
DIQAKLGTDYRL RLGLGHPGDR NLVVGYNKPST EXPPTDXRCRR QIPASHTRHPCR
|||||
g616          130     140     150     160     170     180
DIQAKLGTDYRL RLGLGHPGDR NLVVGYNKP SAEAPPANRR CRRIQAGRTR HHFR

m616.pep      190     200     210     220     230     240
QMGRSNPLPAQ QMTRCRLKPF QTACSRFPYPS HORTQAAYPN RIHPRHRNRN PRFPALRM
|||||
g616          190     200     210     220     230     240
QMGRGNALPAQ QIIQCR LKPFQTAFS RFYPNSHERT QAAYPNGIHP RHRRNPRFFA VRM

m616.pep      250     260     270     280     290     300
QHRCPLRRRNCR LARYAGRTRR KIPAPIQTMPD MAXRGTSMNL PRNRFILLSA LWFAGS
|||||
g616          250     260     270     280     290     300
QHRNSTVRRRS GTMARHTCTR RQIPAPVQNL PNVAGRGGMK LPRNRFSLSA LWFAGG

m616.pep      310     320     330     340     350     360
IYSLLFKAAETAP PPFPHFDKVA HLAFFAQIWL TKAFRTDNRPI PYRSLMVFALC FAL
|||||
g616          310     320     330     340     350     360
IYSLLFKAAETAP PPFPHFDKAA HLAFFAQILF LAKAFKTGKLP IPIYRSLIAFA FCFAV

m616.pep      370     380     390     400
FSECAQAWFTAT RTGLGDVLAD LTGAALALFT ARAACRPDX
|||||
g616          370     380     390     400
GSECAQAWFTAT RTGLGDVLAD LTGAALALFA ARSACRPDX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq
1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATTT CTTCGGCGAA
151 GTCGCCCCGTG CTACCTGCCG CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAAAT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTGAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGTT TGCCGGCGGC
901 ATCTATTGCG TGCTCTCAA AGCTGCCGAC ACCGCGCCG CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTTCGCA CTCTTTGCCG CCCGCGCCG CGACCGCCCG
1201 GACTGA

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
51 VARATLPDGD VWLLKPTTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTTRCLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPREFAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLTKAFK TGKLPPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSGLDV LADMAGTVLA LFAARAADRP
401 D*

m616/a616 90.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
a616	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
a616	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
a616	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
a616	190	200	210	220	230	240
	250	260	270	280	290	300

m616.pep	QHRRCP LRRRNCRLARYAGRTTRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
a616	QHRRRTIRRRSGT MARHTCTRRRI PAPVQNLPN VAGRGGGMKLPNRNFSLLSALWFAGG
	250 260 270 280 290 300
	310 320 330 340 350 360
m616.pep	IYSLLFKAETAPPPFP HFDKVAHLALFFAQIWLLTKA FRTDNRPIPYRS LMVFALCFAL
a616	IYSLLFKAADTAPPPFP HDKAAHLALFFAQIWLLTKAF KTGKLPIPYRS LMVFALCFAL
	310 320 330 340 350 360
	370 380 390 400
m616.pep	FSECAQAWFTATRTGS LGDVLADLTGAALALFTA RAACRPDX
a616	FSECAQAXFTATRTGS LGDLADMAGTVLALFAARAAD RPDX
	370 380 390 400

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g619.seq
1    ATGCGCGTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGTCGGTT
5    CGGGGTCGCC  TTTGCGCTGT  TGCTGGTTTC  TGCATCTCTG  TTTATGACGC
101  TCAACGTCAA  AGGAGATTGG  GACTTTGTCT  TGCACCTGCG  CCTGACCAAG
151  CTTGCGCGCG  TGCTGATGGT  CGCCTATGCG  TCGCGCGGTG  CAACTCAACT
201  CTTCCAACAG  CTGACAACAA  ACCGATTTCT  GACCCCTTCG  ATTTTGCGTT
251  TCGATTTCGT  GTATGTGTTT  TTGCAGACCT  TGCTGgtGTT  TACGTtcgGC
301  GGGCTGGGCT  ATGacatccg  cgcggtgact  gGCAAATTCT  GCTTTGAACT
351  GGTGTGTATG  ATGAGCGGCT  CGCTGCTGCT  GTTTTACACG  CTATCCCTGC
401  AGGGCGGGCG  CGATTTGCCG  CACATGATTT  TAATCGGCGT  GATTTTCGGG
451  ATTTTGTTCG  GCAGCGCTTC  CTCGCTGCTT  TCGCGCATGA  TAGACCCCGA
501  AGAATTATCC  GCGCGCGAGG  CGAATATGTT  TGCCGGATTT  AATACCGCTG
551  GCAGCGAGCT  TTTAGGCATA  GGGCGCGCTG  TCCTGCTCGT  CAGCGCGGCG
601  GTGCTTTGGC  ACGAATGCGA  CCGCTCGGAG  GTACACCTTT  TGGGCGCGGA
651  CCAAGCCGTC  AATTTCGGCA  TCAGCTACAC  GCGCAACACC  TTATGGATAC
701  TGCTTTGGAT  TGCCGCATTG  GTGGCGACGG  CGACCGCCGT  TGTGGGCCCG
751  GTGAGCTTCT  TCGGGGCTTC  CGCGCGCTCG  CTTGCGCAAC  ACTTTTCCCc
801  gtCCGTCGCG  CATTCCGCTG  GCGCTGCgat  gacggttGc  gtcgGggcGA
851  TCCTCTTGgt  cggCggacaA  ACCGTATTCT  AACACTTCTT  GGGCATGAag
901  gCggtATTAA  CGGTGGTGGT  cgAATTTGCG  ggcggaactc  TTTTCTCTA
951  TCTCGTTTTA  AAACACAAAA  AATGA

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g619.pep

1	MPSEKNIGFM	AGSSRPLRVA	FALLLVSCIL	FMTLNVKGDW	DFVLHLRLTK
51	LAALLMWAYA	VGVSQTQFQT	LTTNPILTPS	ILGFDSLXYF	LQTLVLVFTFG
101	VGQYTSPLPT	GKPGFELVVM	MGGSLLLEYT	LIRQGRDLPI	HMILGLVIFG
151	<u>ILVRSLSLL</u>	SRMLDPEEFT	AAQANPMFAG	NTVRSSELLGI	GATVLVLSVA
201	<u>VVWHERYRSD</u>	VHLLGRDQAV	NLGISYTRNT	LWILLWIALI	VATATVAVGP
251	<u>VSFEGFLAAS</u>	LNHNFSPSVR	HSVRLPMTVC	VGGILLVGGQ	TVFEHFLGMK
301	AVLSVVEFEA	GGVLVLYLVL	KHKK*		

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m619.seq
1  ATGCGCTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGCCCGTT
51  GTGGGTCGCC  TTTCGCCTGT  TGCATGGTTT  TCGCGTCCTG  TTTATGACGC
101 TCAACGTCAA  AGGCGATTGG  GATTTTGTGT  TCGAACTGCG  GCTGACCAAA
151 CTTGCGCGCG  TCGTGATGGT  CGCCTATGCG  GTCGGCGTGT  CCACGCAACT
201 CTTCCAAACG  CTAGCAATA  ATCCGATTGT  GACCCCTTCA  ATTTTGGGTT
251 TCGATTTCGT  GTATGTGTTT  TTGCAGACCT  TCGTGGTGT  TACGTTCCGC
301 GCGGTGGGCT  ATGCTTCCCT  GCCGTGACG  GGCAAATTCG  GCTTTGAART
351 GGTCGTCGAT  ATGGGCGGCT  CGCTGCTGCT  GTTCTACAGC  CTCATCAAA
401 AGGGCGGACG  CGATTGTGCG  CGCATGATT  TAATCGGCGT  GATTTTCGGG
451 ATTTTGTTC  CGAGCCTGTC  GTCGCTGCT  TCGCGCATGA  TCGATCCCGA
501 AGAATTTACC  CCGCGCAGC  GGAATATGTT  TGCCGGATT  AATACCGTCC
551 ACAGCGAGCT  TTTGGGCATA  CGCATCGTGA  TTCTGCTCGT  CAGCGCGGCC
601 GTCGTTTGCG  CGGAACGCTA  CCGCTTGAC  GTTTACCTTT  TGGGGCGTGA
651 CCAAGCCGTC  AATTTGGGCA  TCAGCTACAC  CGCACAACCT  TATATGGTAC
701 TGCCTTGGAT  TCGCCGATTG  TGCGGCACGG  CGACCGCGGT  GGTGCGCCCC
751 GTAAGCTTTT  TCGGGCTTCT  CGCGCGCTCG  CTTGCCAACC  ACTTTTCCCC
801 GTCGCTCAA  CATTCGCTTC  GCCTGCGCAT  GACGGTTTGT  ATCGCGCGCA
851 TCCCTTTGGT  CGCGCGACAG  ACCGTGTTGC  AACACCTGCT  CGGTATTCAG

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992

901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTCTCTA
 951 TCTCGTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNKGDW DFVLQLRLTK
 51 LAALMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLVFTFG
 101 GVGYSPLPT GKFGFELVVM MGSSLLLFYT LIKQGGRLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNKGDWDFVLQLRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYTSLPLTGKFGFELVVM					
m619.pep	130	140	150	160	170	180
	MGSSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGSSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAVVWHERYSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHVSRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKKK					
g619	AVLSVVVEFAGGLVFLYLVLKHKKK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTG AAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTGGGTT
 251 TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGGC
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCTTATG ATGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGGCGGGCG CGATTGCGG CGTATGATT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTC GCAGCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA
 501 AGAATTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTT TGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCGCT TGTCGGCCCG

993

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751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTTGCG GGCGGACTCG TTTTCCTCTA
951 TCTCGTTTTA AGACACAAA AATGA

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This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGDLPL RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

      10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
a619      MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
      10      20      30      40      50      60

      70      80      90      100     110     120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
a619      VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
      70      80      90      100     110     120

      130     140     150     160     170     180
m619.pep MGGSLLLFYTLIKQGGDLRMLIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619      MGGSLLLFYTLIKQGGDLRMLIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      130     140     150     160     170     180

      190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619      NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m619.pep VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619      VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
      250     260     270     280     290     300

      310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKXX
a619      AVLSVVVEFAGGLVFLYLVLRHKKX
      310     320

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

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This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDGMNVDWTDNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```


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m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTL	LAIVAV	SALSAC	RAEEGP	PLPRQI	SDRSVGHYCSMNLTEHNGPKAQIFLNGKP
a620	MKKTL	LAIVAV	SALSAC	RAEEGP	PLPRQI	SDRSVGHYCSMNLTEHNGPKAQIFLNGKP
	10	20	30	40	50	60
m620.pep	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNVTDWTFNPNADTEWMDAKKAFYVIDS
a620	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNVTDWTFNPNADTEWMDAKKAFYVIDS
	70	80	90	100	110	120
m620.pep	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNVTDWTFNPNADTEWMDAKKAFYVIDS
a620	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNVTDWTFNPNADTEWMDAKKAFYVIDS
	70	80	90	100	110	120
m620.pep	GFIGGM	GAEDAL	PFGNKE	QAEKFA	KDKGGK	VVGFDDMPDITYIFKX
a620	GFIGGM	GAEDAL	PFGNKE	QAEKFA	KDKGGK	VVGFDDMPDITYIFKX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta cgcgtgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTCCG CGTTGCCTGC
301 GGCTTGATT CGATGGTTT GGGCGAGCCG CAGATTTTG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCCGTTG CTAAGAAGT CCGTACCGAT
451 ACCGCTGTCG GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGGAAACAG ATTTTCCCG ACATCGGCGA TTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCAGGCCAG
751 CTTCCGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaaag ccgcccgcCgc
951 cgccgaaacg ctggTGTCGG AAAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGGCAGGCA GagcgttcCG CTGATTAAAG CCTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GAAAAATGCG ATGAAACAGC TTGCCAAAAGG
1101 CGcaaCGGCG GAAGaggttt TGgaacggct gtccgctCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAAT CAAACCTTGA ATAAGGCGGG GGAAGAAAGT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDME TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESM AKLNALFQRT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRIMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCTAAA GCCGTCCGCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC

```

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```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501 GCGCGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAAG CATGGTGGAG CGTGCATTGA AACAAAGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGCGGGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

```

m622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

m622/g622 98.8% identity in 415 aa overlap

m622.pep      10      20      30      40      50      60
MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
|||||
g622          10      20      30      40      50      60
MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD

m622.pep      70      80      90      100     110     120
SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
|||||
g622          70      80      90      100     110     120
SEEIIRWLADYHSLPIEEIRPYLYTLDMEQETVRHAFRVACGLDSMVLGEPQILGQIKDAV

m622.pep      130     140     150     160     170     180
RVAQEQESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
|||||
g622          130     140     150     160     170     180
RAAQEQESMGAKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV

m622.pep      190     200     210     220     230     240
LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY
|||||
g622          190     200     210     220     230     240
LFIGAGEMIELVATYFAAKNPRMLTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY

m622.pep      250     260     270     280     290     300
DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLDAYLYTVDDM
|||||
g622          250     260     270     280     290     300
DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLDAYLYTVDDM

m622.pep      310     320     330     340     350     360
VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA
|||||
g622          310     320     330     340     350     360
VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA

m622.pep      370     380     390     400     410
MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX
|||||
g622          370     380     390     400     410
MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX

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370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCCTCAT GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAG CCGCCGCCCG
951 CGCCGAAACG CTGGTGTCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGTTG TTCACGCCGT CGCGCAGATT TATCATTGTTG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQUESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQGGRQSVF LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAAAACLPFAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEQUESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEQUESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNLNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATAC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG
 151 CACcgGCacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGC CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatcctTTtg CatTTTCccc aacnctgggtg ggtcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CTTGTGcac ATacggatgt gGcacAGacC
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPOXWWVGA
 101 VSSVFCSLVT IRMWRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCTCC TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATGC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGC CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGCGGGCG
 301 GTTTCATCGG TTTTGTGTC CTTGTGCGC ATATGGATGT GGCGCAGGCG
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMEW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLGIIG IFPLPLPTTP FVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g624           HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1  ATGATACGTT ATCTTTTAAAT TGCCTGCGGC TGCATTTCCTG TCGTGTGGG
51 TATCATCGGC ATTTTTTTGCG CGCTGTGCGC GACCACGCCG TCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTGGGGCG
301 GTTTCATCGG TTTTTGTTC CCTTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624           MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624           HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCTGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGtTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtaa

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPME ASAVPTASRA

```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTGCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCCGTCC TGAGCATTC TGAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501  GGTCaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551  ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601  ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1  MSGWLKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51  FNFEPIAEVG KFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201  TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101  CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151  TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201  CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251  CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301  AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351  CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401  CCTTGATGAC GGGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
451  TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501  GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTTCG
551  GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601  ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1  MSGWLKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51  FNFEPIAEVG KFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201  TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10          20          30          40          50          60
m627.pep  MSGWLKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||
g627       MSGWLKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10          20          30          40          50          60

```

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINTMYFWMSGILSAFLDNAPT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTL	IFFVFKLLX				
g627	TFFRYMMWSVAFLTPVFIVHTL	LVFFVFKLLX				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCCTG TTTTATTGCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVS	LVHDTAGHPINVMYFWMSGILSAFLDNAPT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMG	SVFMGALTYIGNAPNFMVKAIAEQRGVPMP				
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTL	IFFVFKLLX				

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
 51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTAC
 101 ACACATGGAT TTTACGTTTC GTCAGGCGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
 301 GATTGAATCA GGTTCGGCGC CACTTTTTCG CTGCTCAATT TTGCCAGCGC
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNLTNRPR
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 AAACATGGAT TTTGCGTTTC GTCAAACGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GGTTCGGCGC CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNLTNRPR
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

		10	20	30	40	50	60
m628.pep		MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLN	TNRPR	PKSSAASLIM	
g628		MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAA	LHTWILRSV	RRLNLTNRPR	PKSSAASLMM	
		10	20	30	40	50	60
		70	80	90	100	110	120
m628.pep		TVGSAASGLVSIALTKMANG	SASTAGILLN	GRVRSVAVHKP	DWIRLRRTSS	PLKFASASGA	
g628		TVGSAASGLVSIALTKMANG	SASTAGILLN	GRVRSVAVHKP	DXIRLRRTFS	LLNFASASGT	
		70	80	90	100	110	120
m628.pep	X						
g628	X						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
  1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
  51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
 151 CTGAAATCCT CGGCGGCTTC TTGATCACA ACCACAGGGT CTGCCGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGGAT TTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
 351 TTCGGGCGCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
  1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
  51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP
 101 DWIRLRRTSS PLKFANASGA *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAP	AALHTWILRSVKRLNTNR	PRLKSSAASLIM		
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAP	AALHTWILRSVKRLNTSKPRLKSSAASLIT			
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSS	SPLKFASASGA			
a628	TTGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSS	SPLKFANASGA			
	70	80	90	100	110	120

```

m628.pep    X
             |
a628         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
  1 ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
  51 ggatatGTTT GCCGTCAGcc tGtcggTCGG cattgccgaT TTCCGCTGGT
 101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
 201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
 251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
 301 ctgctgectg CcgcGccgct gccggtcaAA ATGTCGGtag Cgcgccgttgc
 351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaataccgC Cgcctgccac
 401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
 451 GttgaGGCGG TGGCAGCAGT TGTGCGGTAT GAGTTTGAGA TGCTGCAAAAT
 501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
 551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTTTGC CTACCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
 651 GGGTTTGAAC CGGACGGCGG TGTGTTGGTC GGGTTTGATT ATTGTGGCAC
 701 TGATTACATC GCTGGTCATT GTAACGCTCG GCAATATTCC GTTTATCGGG
 751 CTGGTCGTGC CGAATATCGT CAGCCGCTCG ATGGGCGACA GGCTGCGCCA
 801 AAGCCTGCCT CCGGTCGCCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG
 851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG
 901 GTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
 951 ACCCGCTAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
  1 MTAKPFSLNL ANLLPAVLV AVLSVGIAD FRWSDVFSLS DSQQVMFISR
  51 LPTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
 101 LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

```

151 VEAVATFVAY EFEMQLMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVPVNIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFFFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

m629.seq

m629.pep

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m629.pep	MTAKPFSNLNLNLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
g629	MTAKPFSNLNLANLLLPVLFPAVSLSVGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
	10	20	30	40	50	60
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQAALGLLLMTLLLPAAPLPKMSVAAVAALI					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIIAYENEMQLMGVWQQGDFSSVL					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMQLMGVWQQGDFSSVL					
	130	140	150	160	170	180
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
g629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	190	200	210	220	230	240

1006

```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
          190      200      210      220      230      240

          250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
          250      260      270      280      290      300

          310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VFGVLGTALFLWLLLRKPAYAVX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCGGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGGCAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTGTGC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGTCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTGTC
351 CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTGC GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACGTGT GTGGGCAACG GGGATTTTGG CTTTGTGTGC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGGTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIGI
251 LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

          10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLLPRTFAIVLT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLLPRTFAIVLT
          10      20      30      40      50      60

          70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMV GASQAALGLLMTLLLPAAPLPVKMSVAAVAALI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQAALGLLMSLLLPAAPLPVKMSVAAVAALI
          70      80      90      100     110     120

          130     140     150     160     170     180
m629.pep  GMLVFMLLRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMGVWQQGDFSSVL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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a 629      GMLVFMMILIRLPPTAQLMVPLVGIIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
              130      140      150      160      170      180

              190      200      210      220      230      240
m629.pep   LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
              ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
              190      200      210      220      230      240

              250      260      270      280      290      300
m629.pep   VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
              250      260      270      280      290      300

              310      320
m629.pep   VFGVLGTALFLWLLLRKPAYAVX
              |||||:|||||:|||||:|||||
a 629      VFGVLGTALFLWLLLRKPAHAVX
              310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattg  tttacggcat
51  gtacaacgtc  GGCGCACAGG  CATTGCGTGC  CTTAACGCCC  GAtttgctgc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  cccccgaaGc  gggcgtgtTg  ggcaaaatgc  tgttcgGCGC
201 GATttacttc  ctgccgattt  acgcgaccgt  aTTTATTGTG  GGcggcttct
251 ggGaaqtCTT  GTTCGCATCc  gtACGCAAAc  ACGAAATCAa  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCGCCCAc  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAa  AACTTCATGa  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTA  CCCCGCCAAc  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAc  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCc  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTtT  GCCCGCATCG
701 CttcttgCGc  CATTATTGcc  ggCGTGATGa  TCGGTatGat  tGcgatgTCT
751 tcgctgatta  acttcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggT  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQQSIAND  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFAS  VRKHEINEGF
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAAHGADGL  KNAVtGQTIT
201 WMDAFIGKLP  GSIGEVSTLA  LLIGGAFIVF  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GCGCGCAGG  CATTGCGTGC  GTTAACGCCT  GATTGCTGTC
101 AACAAAACAT  CGCCAACGAC  TGGCATTACG  CCTTGCCAAc  CGCTTTGGGC
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTcG  GACAAAATGC  TGTTTGCGCG
201 GATTTACTTC  CTGCCGATT  ACGCGACTGT  ATTTGTTGTG  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAc  ACGAAATCAa  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCGCCCAc  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAa  AACTTCATGa  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTA  CCCTGCCAAc  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAc  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCc  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTtT  GCCCGCATCG
701 CTTCTTGGCG  CATTATTGCC  GCGGTGATGa  TCGGTATGAT  TGCGATGTCT
751 TCGCTGTTCa  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

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801 TTGGTACTGG CACTTGGTGG TCGGCGGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCTGTCTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTTG
 1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVEVV GGFWEVLFAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLNFFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVVPAYP EGMLLAILFA NLFAPIFYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQONIANDWHYAFANALGINMSSEAGVS				
g630	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQSIADHGNALANALGINMSPEAGVL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLNFFIGSDTNAMFAMPWYHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLINFIGSDTKAMFAM---HLVHGTTWKDDYHSLYIK.					
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVPAYPEGMMLAILFANLFAPIFYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GCGCACAGG CATTGCGTGC GTTAACGCCC GATTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GCGAAAATGC TGTTGCGGCG
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GCGAAGTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGCGGTT GACGCTATT CCGCGCAAC CGCGCTGGCG CAATGGCGCG
 551 CACACGGTGC AGACGGCCTG AAAAACGCCA TAACCGGTCA AACCATCACT
 601 TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTC AACTCATCGG TCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTG
1001 CCCCATTTC CGACTATTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYAFANALGINMSSEAGVS					
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYALANALGINMSSEAGVL					
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
a630	GKMLFGAIYFLPIYATVFIVGGFEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLENFIGSDTNAMFAMPWYHVLVGGFAIGMLFMATDPVSASFTNVGKWW					
a630	GVMIGMIAMSSLENFIGSDTNAMFAMPWYHVLVGGFAIGMLFMATDPVSASFTNVGKWW					
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTAGATA CACGATGACG
101 GGGATTTC AACTGCGCAG CTGTTGCGAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTT CTTACCCAGT TTTTCCAACA CTTCTCTTC CGTCAGCTTT
251 TGCCCGTAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG

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```

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
401 GCAGCATTC AAGGATAAGA CAAGGGTCTG TACCAGATTA G

```

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

```

g635.pep
1  MTRRRVGKQN RIAIHSAYR KMVVFVFIQI HDDGDFQLRE LFERQGIQIAFR
51  LKTQIGHNAP HILKRRALHF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG
101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCISQITIR QGSVPD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

```

m635.seq
1  ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
51  GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTTCGC
151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCCTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGGA
301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

```

m635.pep
1  MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQIAFR
51  FKTIQIRHAP HILKRRGHLI LIQFF*HVLV RQLLPVKIVQ KRRHRSRPAG
101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

```

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFIQIHDDGDLQLCKLLERQGIQIAFRFKTIQIRHAP					
g635	MTRRRVGKQNRIAIHSAYRKMVVFVFIQIHDDGDFQLRELFERQGIQIAFRKLTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLILLIQFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
g635	HILKRRALHFLTQFFQHFFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIPPRFPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSISNRIIVKHRCISQITIRQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

```

a635.seq
1  ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
51  GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTTCGC
151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCCTCTTC CGTCAGCTTT
251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGGA
301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

```

a635.pep
1  MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQIAFR
51  LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*

```

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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```

m635.pep  MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
a635      MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDAP
           10      20      30      40      50      60

           70      80      90      100     110     120
m635.pep  HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635      HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
           70      80      90      100     110     120

           130
m635.pep  DFSISNRIIVDX
a635      DFSISNRIIVDX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTGGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCGccggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATACGGAAA CCGCTGAAA CGGTACGGCA ACGCGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFFEINT GIHCWQAHTG TGNQVQAERY
201 VRRVYGYGTF ALVPFDGCGT VGRPFNRNRF VDIKFLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHVSPLF
301 RSVWPNKIKH HSNVPVFIAK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCCT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTGGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCCAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

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This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```

m638.pep
  1  MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101  IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151  RTMQIYADRI IQNIVVFNQG ARGSSFFEINT GIHCGQAHTG TGNQQAERY
201  VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251  GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

      10      20      30      40      50      60
m638.pep  MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI
g638      MIGGQFIVVG IVGNALARF VDNVVVNIGI VDIVEHDALI AAADGDIVER FEFFGKHQHI
      10      20      30      40      50      60

      70      80      90     100     110     120
m638.pep  AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG IGKNAVPPFG NVVADDLRTG
g638      AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG IGKNAVPPFG NVVADDLRTG
      70      80      90     100     110     120

      130     140     150     160     170     180
m638.pep  CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNQG ARGSSFFEINT
g638      RVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNQG ARGSSFFEINT
      130     140     150     160     170     180

      190     200     210     220     230     240
m638.pep  GIHCGQAHTG TGNQQAERY VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA
g638      GIHCGQAHTG TGNQQAERY VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA
      190     200     210     220     230     240

      250     260
m638.pep  GSQFERIARP GAGKCGIPIS IIGS*
g638      GSQFERIARP GAGKCGIPIS IIGS*
      250     260     270     280     290     300

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```

a638.seq
  1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101  TTGAGCATGA TGCTTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151  TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201  AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251  AAACGCAAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301  ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351  GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTCCAG
401  CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451  AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501  CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551  GCGGCGAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601  GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651  TTGACAGACG GTCGCGAGGC CCTCAATCG TAATCGGTTT GTCGATGTGA
701  AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751  GCGCGGGGCA AATCGGGAT ACCGATCAGC ATAATCGACT CATGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```

a638.pep
  1  MIGGQFIVVG IVGNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101  IGKNAVPPFG NVVADDLRTG RVPNGNAVAA LVHAQSRVAD DFILPHHRIG
151  RTMQIDADRI IQNIVVFNQG ARGSSFFEINT GIHCGQAHTG TGNQQAERY
201  VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP

```

1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVNVNIGIVDIVEHNALIAA	ADGDIVEYFEPLGKHQHI			
a638	MIGGQFIVVGIVGKNALARFV	DNVNVNIGIVDIVEHDALVAA	ADGDIVKHFEPLGKHQHI			
	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVVFGVVR	AGIGKNAVPPFGNVVADDLRTG			
a638	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVVFIGVVR	AGIGKNAVPPFGNIVADDLRAG			
	130	140	150	160	170	180
m638.pep	CVPNGNAVALVHAQSRVADDF	ILAHHRIGRTMQIYADRIIQNI	VVFNQGARGSF	FEINT		
a638	RVPNGNAIALVHAQSRVADDF	ILPHHRIGRTMQIDADRIIQNI	VVFNQGARGSF	FEINT		
	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVAERYV	RRVYGYGTPAPVAFDGGCGTV	GRPFNRRFVNVKFGFIYA			
a638	GIHCGQAHTGTGNGQVAERYV	RRVYGYGTPAPVSFDGCRTV	GRPFNRRFVDVKFGLIYA			
	250	260				
m638.pep	GSQFERIARPGAGKCGIPISI	IGSX				
a638	GSQFERIARPGAGKCGIPISI	IDSX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCTG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGCGGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GCGAAGTGCG TTTTTCCTTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTTCCCGCGG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGGAACAC GGTCTTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AOVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGGYV LMFSERLKVF DNIIVGSRD*
151 GIMLVVNYD DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQV YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAATGCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTACAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCACAAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACT CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAA
651 CCGAGTCAA TACGTACGCA CGCGCTTCT CGATTGGAGC GAGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CCGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAAC CCGCAGTCGG
1001 AATGGGCGAG GCGGAAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFAVHYM YTNDSSEISN ISVGNMNGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMNGYVLMFSERLKVFNDIAGVSRDXGIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVFNDIAGVSRDQGIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDAYRPNQIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLEKETVROSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLEKETVROSERGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

1015

```
1  ATGAGCCTGC  CCGCAATGGA  TGCCGGTATT  TATCTCGAAG  AAACTGCCCC
51  GCGCGCCCTG  ATTGAACACA  ATAATATTTT  GGATAATTCG  GTCGGCGTCT
101 ATCTGCATGG  TTCTGCCGAT  GCGATGGTGC  GGGAGAATAA  AATCGTCGGC
151 GACGCGACTT  TGCGCGTGAA  CGAGCGCGGC  AATGGCGTTA  CCGTTTGGAA
201 CGCGCCCGGC  GCGCAGGTCG  TCGGCAACGA  TATTTCCAAA  GGGCGGGACG
251 GCATTTTTC  CAATACCAGC  ACGCACACA  CCTATAAAA  CAACCGCTTC
301 AGCGATTTC  GTTTCGCCGT  CCACTATATG  TACACCAACG  ACAGCGAAT
351 CAGCGGCAAT  ATTTCCGTGG  GCAACAATAT  GGGCTATGTG  CTGATGTTT
401 CCGAGCGGCT  CAAAGTGTT  GACAATATCG  CCGTCGGCAG  CCGCGACCAA
451 GGCATCATGC  TCAACTATGT  CAACTATTCC  GATATTCACG  ACAACATTAT
501 CAACAAAGCG  GGCAAGTGC  TTTTGCCTA  CAATGCCAAC  TACGATAAAC
551 TGTCCGCCAA  TCATTTTGAA  AACTGCCAAA  TCGGCATACA  CTTTACCGCC
601 GCCATCGAAG  GCACGTCCCT  GCACGACAAT  TCCTTTATCA  ACAACGAAAG
651 CCAGGTCAAA  TACGTCAGCA  CGCGCTTTCT  CGACTGGAGC  GAGGGCGGAC
701 ACGGCAACTA  TTGGAGCGAC  AACAGCGCGT  TCGATTTGAA  CGGCGACGGC
751 TTCGGAGACA  GCGCGTACCG  TCCCAACGGC  ATCATCGACC  AAATCATCTG
801 GCGCGCACC  GTATCGCGCC  TCTTGATGAA  CAGTCCCGCA  ATCAGCATCG
851 TCAAAATGGC  GCAGGCGCAA  TTCCCGCCG  TTTTGCCTGG  CGGCGTGGTG
901 AIEGTSLHND  SFINNESQVK  YVSTRFLDWS  EGGHGNYSW  NSAFDLNGDG
951 TCAGGCGATG  AAGGACGGGC  TGCTCAAAA  AGTCGAAACG  CGGCAGTTGG
1001 AATGGGGCAG  GCGGAAAAAC  GGTTCTTTGA  ACTAG
```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```
1  MSLPAMDAGI  YLEETAPRAL  IEHNNILDNS  VGVYLHGSAD  AMVRENKIVG
51  DATLRVNERG  NGVTVWNAPG  AQVVGNDISK  GRDGIFSNTS  THNTYKNNRF
101 SDLRFVHYM  YTNDSEISGN  ISVGNMGMV  LMFSERLKVF  DNIIVGSRDQ
151 GIMLNYSY  DIHDNIINKA  KGCVFAYNAN  YDKLSANHFE  NCQIGIHFTA
201 AIEGTSLHND  SFINNESQVK  YVSTRFLDWS  EGGHGNYSW  NSAFDLNGDG
251 FGDSAYRPN  IIDQIIWRAP  VSRLLMNSPA  ISIVKWAQQA  FPAVLPGGVV
301 DSKPLMKPYA  PKIQTRYQAM  KDGLLKKVET  RQLEWGRAEN  GSLN*
```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNMGMVLMFSERLKVF DNIIVGSRDQGIMLNYSYDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGMVLMFSERLKVF DNIIVGSRDQGIMLNYSYDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGFSGDSAYRPNIIIDQIIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNIIIDQIIWRAPVSRLLMNSPAISIVKWAQQAQFPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCTCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CCGGTGTGGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCCCGGGC GACATCATCA GcggTGGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCCGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAG
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTGAGCCAGC CTCCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCGG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCCGGTT TTAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTGACGGT GCGGAGCCGT GCGGCGTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201 GSKALQTAS ASDVREAAPA SETPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGD PD FIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRTDAQH ERVVELSAAD APRFEVSWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCTCTGT TTTTCAATCA AACGTATGTC CCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKMSAFRRARITAFFAAAFVFLTAALPAYAERLPDFLAK					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||
g640           IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||
g640           DGTIAGAKLVDHHEPIMLIGIPQSRVDFIDKYIGLNFNIKNPPTPSVAPGDIISGATVTL
                130      140      150      160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCGTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFFAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRRITAFFFAFVFLTAALPAYAERLPDFLAK
                |||
a640           MIHIISILKSIGISGIVMSCFSIKRMSAFRRITAFFFAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||
a640           IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130      140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||
a640           DGTIAGAKLVDHHEPIMLIGIPH
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1  ATGCGGTATC CGCCGCAATC GGC GGTTTTC CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTGCCCG CTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCTCTCCT GTACGAAAGC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgTCgc gGGCAACGGC
301 GGcaaagcgc ACatcggtTT Gcacggcgtc gagCAGGGgt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAAGTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGCGCGATA TCGATGGCGA TATTGCCGCG TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGCGGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTCCGCGC GTTCGTAATC GACGAATCTG

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1018

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701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCAGCGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTGCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgc Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTGCGCGC
1051 GttgACGTAA ATGGTTtgtt cgtcggata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCcgcgccg gaggtTtcgg gttcggtaAc gccccaaacgg
1151 cggcttttcgc ctTTGAAAAT CATGTCCAAA CCTGTGCGCA CTTCGccttc
1201 gccgcccgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADV VQEGC
51 GV FVFLLYED KKS GDDFADE DFLQAGVVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEF LQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGF GFGN AQTA AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAAC TTCA TGCCTGCTTC
301 TTTTCTCTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGA TTCGTGCGC AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCGC
601 GATTTCCGGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTGCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCAGAGTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQEGCGVVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSFQI FKDVFNHNAV HADQLQAAAD KDV LERAQTG
251 SVALGEFHGG GCRHFGIDAV DGVT DGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```


1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVFR	LYED	
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVFR	LYED				
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQGAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQGAGVGGVFLQEAADVFGQSVVAGNGGKADIGLHGV	EQGLV	FVQLN				
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVDSIAGGVSAFKTLRTQEF	LQHLRG					
g642	ACFFFFGGGDELVVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEF	LQHLRG					
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKKNLGNLMAAPDFAAFV	IDEF	VDVADV				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFV	IDES	DIVADIS				
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQTSVALGEFHHGGCRHFGI	DAVDG	VTDGA				
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQTSVAPGEFHHGGCRHFGI	DAVDG	VTDGA				
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRG	VDVNG	LSVDI				
g642	QAFGCEGFADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRG	VDVNG	LFVGI				
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGLHFACNRRAGGFGFGNTQTAALAFENHLQTLRDLRFIAELLQWLQ	HQRAFD	AGTQR				
g642	FVAGLHFACNRRAGGFGFGNAQTAAFAFENHVQTLCDLRFIAELLQRLQ	HQRAFD	AGTQR				
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

1	GCCTGCCGCC	GTATTTGCC	GCTATCCGCA	ATATCGGCAG	TCCAATATGT
51	CTTTGCCGAT	GTCGTTCAGC	AGGAAGGCTG	CGGTGTCTTC	GTGTTCCGCC
101	TGTACGAAGA	CAAAGAGTCG	GCGGATGATT	TTGCCGATAA	AGACTTTTTC
151	CAGGGCGCAG	GCATCGGTCA	GGGTGTGTTC	CTGCAGGAAG	CTGCGGATGT
201	CTTCGGGCAA	AGTGTAGTCG	CGGGCGACGG	CGGCAAAGCG	GGCATCGGTT
251	TGCAGGCGGT	CGAGCAGGGT	TTGGTTTTCG	TCCAACCTCA	TGCCTGCTTC
301	TTTTTCTTCG	GCGGTGGCGC	GGACAACTG	GTCGTAAT	TGGGCATAAA
351	GCAATATCGT	CGGGCCTTCA	AAAATCGTGA	AGGGGCGGAT	GTCGATAGCG
401	ATATTGCCGG	CGGTGTGTCC	GCGTTCAAAA	CCCTTCGCGC	CCAAGAGTTT
451	TTGCAACATT	TGCGCGGCGG	CGTAAGTGTA	TTCCGTGGCG	AGGGTTTTCG
501	CGATGTTTCG	CTCCATCAGT	TGATGGGCGA	CGGGTGCAAC	GGGCGAAACG
551	GAATGGCAGA	CGTAGCGGTA	AAGAATCTCG	GAAACCTGAT	GGCGGCGCCG
601	GATTTCCGCG	CGTTCGTAAT	CGACGAATCT	GATGTCGTTG	CGGACGTATC
651	GTTCCAGGTT	TCAAGGGTG	TATTCATAA	TGCCGTGCGT	CATGCCGATC

1020

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701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVVS AFKTLRAQEF
151 LQHLRGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTGGAQAF GCEGFAADVC FGDEQQVDDF
301 GFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLHFSGNRR
351 GGFSGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLSAISAVQYIFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLHACFFFFGGGADKLNVNFGIKHIV
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642          70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVVFVQLHACFFFFGGGADKLNVNFGIKHIV

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRTQEFQLHRLGGVSVFRGEGFDDVRLHQLMGDGCN
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642         130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRAQEFQLHRLGGVSVFRGEGFDDVRLHQLMGDGCN

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD

m642.pep     250     260     270     280     290     300
KDVLERAQTGSAVALGEFHHGGCRHFGIDAVDGVTGGAQAFGCEGFAADVCFGDEQQVDDF
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642         250     260     270     280     290     300
KDVLERAQTGSAVALGEFHHGGCRHFGIDAVDGVTGGAQAFGCEGFAADVCFGDEQQVDDF

m642.pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVDIFVVGHLHFACNRRAGGFGFGNTQT
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVDIFVVRHLHFSGNRRAGGFGFGNAXT

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP
|||||  ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

```
g643.seq
1  ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagATGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
351 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a
```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

```
g643.pep
1  MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGMTCA SVAVWVSDGM AVCFSV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

```
m643.seq
1  ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A
```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

```
m643.pep
1  MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*
```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFGMTCA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
g643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
1  ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCCCGGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1  MVLPLMLLAT IRSATLTL*R LAMLRNVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVVWSDGM AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLAT	IRSATLTLXRL	LAMLRNVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRTRR
a643	MVLPLMLLAT	IRSATLTLXRL	LAMLRNVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRTRR
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAE	ILCSATVSGV	PMTAEMVSSA	CRRLFRATSC	MSSSAACMS	FWGMICA
a643	LPSAATVCCGDE	EMLCSATVSG	VPMTAEMVSS	ACRRRLFRAT	SCMSSSAAC	MSFWGTICA
	70	80	90	100	110	120
	130					
m643.pep	SVAVVWSDGM	AVCFSVX				
a643	SVAVVWSDGM	AVCFSVX				
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1  ATGCCGCTCG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTcCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGGA CATGATTTTC AAaggcgaaa gccgcggttt
501 gggcgTtacc gaacccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaAA CCATTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTectcg ttgccgcaaa
651 agagcgcaaaa aacGGcaaac tcgcaaaagt CATCGACCTG CTGCTCGTCC
701 CCAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCCGGGGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTCCGAAA
1001 TCCTTTACCG CTACGTCTGC CATTCGGTTT CGcccgtegc GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
1101 TTAcgcCGCC GCGCAARTGT TGCAAAAAC CTTGGGCGCG AAGGGTTTG
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACA TATGCTTTAT GCCGAAATTT ACGACCAAGT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgacgccc gtgCAAAccg atGTCCgctt tgcCGCGGTT
1351 GCCcgGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

```
1451 TCGGCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

```
g644.pap
1  MPSERPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFEGEA
151 QVAQGLDMIF KGESRRLGVT EPETSGAIIA REMQSCYEYI DEQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSL QLIGMTHGIM
301 EYILDNLNRY VRNDIRFVDY ERREIQRHQQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHAPG NIAIDIRPFT
401 IFEGPNMPLY AEIYDQFVRA TAEKEEAGIK LDKNQTLDDA VQTDVRFPAV
451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
501 FLNDIRKDI LDCRYCG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

```
m644.seq
1  ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAGACACA TCGAATCCGC
201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCC
251 AAGACAAATG GCTTGCTTGC AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAATAA ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAAT
351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTTC CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAAGTCGCG AAGGTTTGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC
551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTACGTT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAA CCGCCAAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAAG CTGCGCGGCC
751 GTCGGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAATAC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCTTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGGCCATCAG GTTCCGAGA
1001 TTCTTTACCG CTACGCTGCG CATTCGTTT CGCCTGTTGC CCCCCTCGCC
1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCG CCGCAAATGT TGCAAAACT CTGGGTGCG AAGGGTTTTG
1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCGCCGCG ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCG GCTCGACCGC CTGCAAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT AACTTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCGTGAC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCGCGCT CTTGTCTTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
1501 TTCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 GTAG
```

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

```
m644.pap
1  MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFEGDEA
151 QVAQGLEMIF KEGGGGLGVT EPETSGAIIA REMQSYEYI DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSL QLIGMTHGIM
301 EYILENLERY VRNDIKFVDY ERREIQRHQQ VSEILYRYVC HSVSPVAPVA
351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHAPG NIAIDIRPFT
401 IFEGPNMPLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLFEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
501 FLNDIRKDI LDCRYCG*
```

m644/g644 94.6% identity in 517 aa overlap

```
10      20      30      40      50      60
m644.pap MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g644      MPSERPADCCPVHFVVKFRKLTNCGRRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
```

1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
g644	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKHGGRKGSQFEIQEVLRI					
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLPLOEFGDEAQAQGLEMIFKGEGGGLGVTEPETSGAAIA					
g644	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLPLOEFGGEAQAQGLDMIFKGESRRLGVTEPETSGAAIA					
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
g644	190	200	210	220	230	240
	REMQSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
m644.pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
g644	310	320	330	340	350	360
	EYILDNLNRYVRNDIRFVDYERREIQRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
m644.pep	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
m644.pep	430	440	450	460	470	480
	TAEKEAGMKLDKNQTLDRLOTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
g644	430	440	450	460	470	480
	TAEKEAGIKLDKNQTLDAVQTDVRFVAARDYALPEDIRSFLQEHTLTDACALQKVFI					
m644.pep	490	500	510			
	GKIIARLFVVFQAKHEDTAFLNDIRKDILDCRYCGX					
g644	490	500	510			
	GKIIARLFVVFQEEHEDTTAFLNDIRKDILDCRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1  ATGCCGTCCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTGCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCTTG AAGCAGGCGG GTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGCGGGCG CAAGGCGAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGCGCG GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGTTTGGA CATGGTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCGGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCCTCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
801 GATGAACTC TCCAGAGCG ACGTGCCGG TTTGCGCGCG TTCCAAACAA

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1025

```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGCCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACCGCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAATT
1251 TGTCCGCGCC ACCGCCGAAG AAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYET DGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HVSVPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

m644/a644 97.3% identity in 517 aa overlap

      10      20      30      40      50      60
m644.pep  MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644      MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
      10      20      30      40      50      60

      70      80      90     100     110     120
m644.pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI
a644      LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGGRKGSQFEIQEVLRI
      70      80      90     100     110     120

      130     140     150     160     170     180
m644.pep  AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA
a644      AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
      130     140     150     160     170     180

      190     200     210     220     230     240
m644.pep  REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC
a644      REMQSYEYTDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC
      190     200     210     220     230     240

      250     260     270     280     290     300
m644.pep  ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
a644      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
      250     260     270     280     290     300

      310     320     330     340     350     360
m644.pep  EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK
a644      EYILENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK

```

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 .pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 .pep	TAEKEAGMKLDKNQTLDRLOTDAFAAVARDYTLPEDIRSFLQEHTLTACALQKVFI					
a644	TAEKEAGMKLDKNQTLDRLOTDAFAAVARDYTLPEDIRSFLQEHTLTACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 .pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a644	GKIIARLFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTGTCTG CAAAAGTTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCTC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CCGCGCAGAC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTGCGACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGCGC AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAA TCTTTAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645.pep

```

1  MMMVLALGMS MPVSMMEQS NTLNLCKKS RMTCSRSSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RKNTPPRLS SRNTASRLP SLNGLTKVFT
101 ARRLGAVVI SEKSRFPSSA MLVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCTC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CCGCGAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTGCGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAA TCTTTAATCA CGGCGCGCAT GCGGCGGCC TGGTCTTCGG

```


1027

851 TTCTCTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

```

m645.pep
1  MMMVLALGIS IPVSMMEQSN TLNRCKKKS RMTCSRSSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPRLS SRNTASRTLP SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTKSUVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

m645.pep	10	20	30	40	50	60
	MMMVLALGISIPVSMMEQSN	TLNRCKKKS	RMTCSRSSR	SCPCATPMRA	SGRVSSRSR	
g645	10	20	30	40	50	60
	MMMVLALGMSMPVSMMEQSN	TLNRCKKKS	RMTCSRSSR	SCPCATPIR	ASGRVSSRSR	
m645.pep	70	80	90	100	110	120
	IFSIVSTSLCRKNTCPRL	SSRNTASRTLP	SLKGLTKVLT	ARRRLGAVVI	SEKSRSPSNA	
g645	70	80	90	100	110	120
	IFSIVSTSLCRKNTCPRL	SSRNTASRTLP	SLNGLTKVFT	ARRRLGAVVI	SEKSRSPSNA	
m645.pep	130	140	150	160	170	180
	ILKVRGIGVAVMVRIST	LARRRLSCSFXRT	PKRCSSSIIT	KPKFLNLMSS	CSTSLCVPITI	
g645	130	140	150	160	170	180
	MLRVRGIGVAVMVRIST	LARRRLSCSFCRT	PKRCSSSIIT	KPKFLNLMSS	CSTSLCVPITI	
m645.pep	190	200	210	220	230	240
	STVPSAMPSSAALVALL	LLKRERLATFTG	KSARKSAKFCA	CCSTKSUVGA	STATCLPPIT	
g645	190	200	210	220	230	240
	STVPSAMPSSVALVALL	LLKRERLATFTG	KSARKSAKFCA	CCSTRSVVGA	STATCLPPIT	
m645.pep	250	260	270	280		
	ATNAARRATSVLPKPT	SPHTRRSIGFAC	VKSLITAAMAA	WSSVSSX		
g645	250	260	270	280		
	ATNAARRATSVLPKPT	SPHTSRSIGFAC	VKSLITAAMAA	WSSVSSX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

```

a645.seq
1  ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCAGCTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGG
851 TTCTTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

```

a645.pep
1  MMMVLALGMS IPVSMMEQSN TLNRCKKKS RMTCSRSSR SCPCATPMRA

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1028

```

51  S GSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLPSLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          MMMVLALGMSIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              10      20      30      40      50      60

              70      80      90     100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLTKVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90     100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRRLSCSEKXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          ILKVRGIGVAVMVRMSTLARRRLSCSEKXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKAFCAACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKAFCAACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVDGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTGVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGTRGFYRIS
101 LII*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : :					
g647	MQRLAADGIQIFFVSVGDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	: : : : :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
201 GGACACCGTT TTTCCGCCAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep
1 VQRLVTHSVQ VFFVGVGDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS
101 LII*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	: : : : : : : : : : :					
a647	VQRLVTHSVQVFFVGVGDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	: : : : :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51 CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
101 GTGGAACA GGTGCGCAGC CGGAATGATA CGCTTGCGTA TGTTGCGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAACCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCATA
301 ATCAAGCTGG CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAA GATTGACCG CCGCCTGAAA
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCCGGA
501 TTTCTGCTG CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCGCG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
101 IKLADTVVFH TAVVFQHQQA FGFDMPOGVE QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	: : : : : : : : : : :					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA					
	: : : : : : : : : :					
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVDLHAI IKLADTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPOGVEQGCRAAAHAAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
	: : : : : : : : : :					
g648	FGFNMPOGVEQGCRAAAHATLRTFRDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
	: : : : : : : : :					
g648	DARALGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCCGGA

```

1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCGCG CATTGATGCC GATGCCCCGA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCT TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAQVDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAAALNQAGVQQAQVDLHAVIKLTDTVVFHAPVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAAALNQAGVQQAQVDLHAVIKLTDTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
m648.pep	FGFDMPQGV E QGCRAAAHATLRTGFDCRLKHFKEGNAAGMPRFAAPDFAVQTSADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCRLKHFKEGNAAGMPRFAAPDFAVQTSADTSGIDA					
	130	140	150	160	170	180
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCAACCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

m649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENKKA RKAFRTLPHY EQKIQCRAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA
 201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

1 MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

m649/g649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN					
g649	MLAILLSAILGLVSTTAAAGTSEPAHRHTKHSKANKQMLHPECRKYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCRAAEYAFDDFDGGSFRRX					
g649	VQELRENKKARKAFRTLPHYAEQKIQCRAAEYAFDDFDGGFRFRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```
a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAAC TGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCCACG CGATACCAA CATATCCGCA
101 AGGCAACAA ACAGATGCTG CACCCCGAAT GCAGGAAATA TTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
201 CAAAAGCCG CGCAAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCAAATGCCG GCGGCGTTAT GAGGCTTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA
```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

a649.pep

1	<u>MLAILLSAIL</u>	<u>GLVSTTAAAG</u>	TSEPAHRDTK	HIRKANKQML	HPECRKYLER
51	RAAWYRSQGN	VQELRENKKA	RKAFRSLPYK	EQKTQCRAAY	EAFDDFDGSR
101	RR*				

m649/a649 96.1% identity in 103 aa overlap

	10	20	30	40	50	60
m649.pep	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECKRYLERRAAWYRSQGN					
a649	MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECKRYLERRAAWYRSQGN					
	10	20	30	40	50	60
	70	80	90	100		
m649.pep	VQELRENKKARKAFRSLPYAEQKIQCRAYEAFDDFDGGSFRRX					
a649	VQELRENKKARKAFRSLPYKEQKTCRAYEAFDDFDGGSFRRX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g950.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCGGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTTG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAAACAA
151 TATTTCCAAT CGGGCAGCCT GTGGGACGCG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAT TGGTACGCGG CCACGAAAGC AAATTCATCG
251 CAAGGCGCAG CTATTTCGAC AGGGTCGTCA ACCGGACGCG ACCCTATATG
301 TACCATTATCG CCAACGAAT CAAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA CGCGGTTCTG CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGGAAA AAACaccgGT TTACGacggc aggcacGacg TTTacgcaGc
501 taccgatgcc gcatCTCAAT AtctGcAATA TTCTATaagg CTGTGTCGGCG
551 ACTGGCGCGT GCGCTTTGCC GCGTCAACT GGGGTGAagg CAACGTCCGA
601 CCGCGCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGGTAT CCCAACGAAA CGCGCAACTT TGTCGCCAAG CTGCTCGCGC
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGCGATGAA TATCAGCGCA

```

1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGCGt tcatCCCCAA AAaCaacgc
901 aaacTGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTGTTT CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCGcgagc gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgcccgc
1251 cgcaCAGACA gcgacatta ccgtcgacc ttgcccga gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcaTt accgaaccgc ccctTGCAGC
1351 AGCCGACGcg CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTCCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTTCATCGAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGGAAC AAACACCGGT TTACGACGGC AGGCACGACG TTACGCGCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ATCTGGCCGCT TGCCCTTTGCC GCCTACAACG GGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCTCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCATTCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCGCG
1251 CGCAGACACA GCGGACATTA CCGTCGCACC TTTGCCGCGA AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGGGAC
1351 AGCCGACGCG CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

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m650/g650 96.1% identity in 465 aa overlap

1034

	10	20	30	40	50	60
m650.pep	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m650.pep	LRQGFMRGEVNPPELVRRHESKFIAHSYFNVRVNRSRPYMYHIANEVKKRNMPAEALLP					
g650	LRQGFMRGEVNPPELVRRHESKFIAHSYFDRVNRSRPYMYHIANEVKKRNMPAEALLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m650.pep	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTKAKSHVGSGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m650.pep	LFGDWPLAFAAYNWGEVNGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
g650	LFGDWPLAFAAYNWGEVNGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m650.pep	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m650.pep	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSIDIDNTPDYRSNMPAGTVNVSIARIQAAAQT					
	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
g650	ADITVAPLPQETVRTGTTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAC  TCAAAACCAT  CGCCCTGACC  GCGTCAGGTC  TGTCCGTTTG
51  TCCGGGTTTC  CTATACGCC  AAAACACCTC  ATCACACCAA  ATCGGTTTGG
101 CGATTATGCG  CTTAAACTCT  TCAATACTCG  ACCTGCCACC  GACAAAACAA
151 TATTTCCAAT  CCGGCAGCCT  GTGGAGCGAG  CTGCGCCAAG  GCTTCCGGAT
201 GGGCGAAGTC  AATCCCGAAC  TGGTACGCCG  CCACGAAAGC  AAATTCATCG
251 CAAGCCACAG  CTATTTCAAC  AGGGTCATCA  ACCGGAGTAG  ACCCTATATG
301 TACCATATCG  CCAACGAAGT  CAAAAACGCG  AATATGCCCG  CCGAAGCCGC
351 CCTGCTTCCC  TTCATCGAAA  GCGCGTTCGT  CACCAAAGCC  AAATCACACG
401 TCGGCGCATC  GGGCCTGTGG  CAGTTCATGC  CCGCTACCGG  CAGGCATTAC
451 GGCCTGGAAG  AAACACCGGT  TTACGACGGC  AGGCACGACA  TTTACGCCGC
501 CACCGATGCC  GCACTCAACT  ATCTGCAATA  CCTCTATGGA  CTGTTCCGGC
551 ACTGGCCGCT  CGCCTTTGCC  GCCTACAACT  GGGGTGAAGG  CAACGTCGGA
601 CGCGCCATCA  ACCGCGCCCG  CGCCCAAGGG  CTCGAACCGA  CCTACGAAAA
651 CCTGCGTATG  CCCAACGAAA  CGCGCAACTA  TGTTCCTAAG  CTGCTCGCCG
701 TGCGCAACAT  CATTGCCGCC  CCCCAATCTT  TCGGCATGAA  TATCAGCGAC
751 ATAGACAACA  AACCGTATTT  TCAGGCAGTC  GAACCGGACC  GTCCGCTCGA
801 CAACGAAGCC  ATCGCCCGGC  TTCCCGGCAT  CACGCAAAGC  GAGCTGCTCG
851 CCCTAAACCC  CGCATTCAAC  GTCCCGCGT  TCATCCCAA  AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVELRRHES KFIASHSYFN RVINRSRPFY
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNVVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

10      20      30      40      50      60
m650.pep MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
|||||
a650      MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
10      20      30      40      50      60

70      80      90      100     110     120
m650.pep LRQGRMGEVNPVELRRHESKFIASHSYFNRVINRSRPFYMYHIANEVKKRNMPAEALLP
|||||
a650      LRQGRMGEVNPVELRRHESKFIASHSYFNRVINRSRPFYMYHIANEVKKRNMPAEALLP
70      80      90      100     110     120

130     140     150     160     170     180
m650.pep FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
|||||
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIAATDAALNYLQYLYG
130     140     150     160     170     180

190     200     210     220     230     240
m650.pep LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAT
|||||
a650      LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAA
190     200     210     220     230     240

250     260     270     280     290     300
m650.pep PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
|||||
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
250     260     270     280     290     300

310     320     330     340     350     360
m650.pep KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
|||||
a650      KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
310     320     330     340     350     360

370     380     390     400     410     420
m650.pep NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT
|||||
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT

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1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCPCDSRSATSNRKTDRAVX					
a 650	ADITVAPLPQKTVRTXTRSPCPYCRTPCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

```

g652.seq
1  ATGATCGAAT TGGACGGTAC TGAACAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCGCG CTACAAGGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCGA ATACTTGGA GGCTTGTTA
551 ACGAATTTCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAACccgG TTCTTTGAGc
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGcgctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

```

g652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDCK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLTEKL GKKVQLVGDD LFTVNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

```

m652.seq
1  ATGATCGAAT TGGACGGTAC TGAACAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATAGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGCGG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAGGCG GCGGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCGA ATATCTGGA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAa CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

```

m652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```

1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

      10      20      30      40      50      60
m652.pep MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
g652      MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
      10      20      30      40      50      60

      70      80      90     100     110     120
m652.pep EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN
g652      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN
      70      80      90     100     110     120

      130     140     150     160     170     180
m652.pep SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
g652      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
      130     140     150     160     170     180

      190     200     210     220     230     240
m652.pep GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
g652      GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
      190     200     210     220     230     240

      250     260     270     280     290     300
m652.pep LLVKVNQIGTLETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
g652      LLVKVNQIGTLETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
      250     260     270     280     290     300

      310     320     330
m652.pep RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGKX
g652      RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGKX
      310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCGCG CTACAAAGCG GGCGAAGACG TATTATTCG ATTGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGCGAAAG TCCAACTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCGGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGTACT
751 TTGAGTGAAG CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
 201 EGWKLLETKL GGKVLVGGD LFTVNPKILA EGIEKGVANA LLVKVNOIGT
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNL	GANATLAVSMAVARAA	EDSGLPLYRYLGGAGPMSL	PVPMNVINGG		
a652	MIELDGTENKGNL	GANATLAVSMAVARAA	EDSGLPLYRYLGGAGPMSL	PVPMNVINGG		
	10	20	30	40	50	60
m652.pep	EHANNSLNIQEFM	IMPVGAKSFREALRCGAE	IFHALKKLCD	SKGFPTTVGDEGGFAPNLN		
a652	EHANNSLNIQEFM	IMPVGAKSFREALRCGAE	IFHALKKLCD	SKGFPTTVGDEGGFAPNLN		
	70	80	90	100	110	120
m652.pep	SHKEALQLMVEATEA	AAGYKAGEDVLFALDCAS	SEFYKDGKYHLEAEGRSY	TNAEFAEYLE		
a652	SHKEALQLMVEATEA	AAGYKAGEDVLFALDCAS	SEFYKDGKYHLEAEGRSY	TNAEFAEYLE		
	130	140	150	160	170	180
m652.pep	GLVNEFFIISIEDGMD	ENDWEGWKLLTEKLGGRV	QVLVGDDLFVTNPKILA	EGIEKGVANA		
a652	GLVNEFFIISIEDGMD	ENDWEGWKLLTEKLGGRV	QVLVGDDLFVTNPKILA	EGIEKGVANA		
	190	200	210	220	230	240
m652.pep	LLVKVNOIGTLSETLK	AVDLAKRNRYSVM	SHRSGETEDSTIADL	AVATNCMQIKTGSLS		
a652	LLVKVNOIGTLSETLK	AVDLAKRNRYSVM	SHRSGETEDSTIADL	AVATNCMQIKTGSLS		
	250	260	270	280	290	300
m652.pep	RSDRMAKYNQLLRIE	EELAEAAADYPSKAAF	YQLGKX			
a652	RSDRMAKYNQLLRIE	EELAEAAADYPSKAAF	YQLGKX			
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA  TCGTTGATAT  TTTCGCCCGC  GAAATTTTGG  ACTCACGCGG
51  CAACCCACAC  GTCGAGTGTT  ATGTATTGCT  CGAATCCGGC  GTAATGGGAC
101  GTGCGGCCGT  ACCGAGCGGC  GCATCCACCG  GTCAGAAAGA  AGCTTTGGAA
151  CTTGCGGACG  GCGACAAATC  CCGCTATTCC  GGCAAAGGCG  TATTGAAGGC
201  CGTCGAACAC  GTCAACAACC  AAATCGCCCA  AGCCCTCATC  GGTATCGATG
251  CCAACGAGCA  ATCTTATATC  GACCAATCA  TGATCGAATT  GGACGGTACT
301  GAAAACAAAG  GCAATTGGG  TCGCAATGCG  ACTTTGGCGG  TCTCTATGGC
351  GGTTCACGCG  GCGCTGCCG  AAGACTCAGG  CCTGCCGCTT  TACCGCTACT
401  TGGGGGGCGC  AGGTCCGATG  TCCCTGCCCG  TACCGATGAT  GAACGTCATC
451  AACGGCGGCG  AACACGCCAA  CAACAGCCTG  AACATCCAAG  AGTTTATGAT
501  TATGCCCGTC  GCGCAAAAT  CTTCCGCGA  AGCGTTGCGC  TGCGGTGCGG
551  AAATTTTCCA  CGCCTTGAAA  AAAGTGTCG  ACAGTAAAGG  CTTCCCGACC
601  ACAGTCGGCG  ACGAAGGCGG  TTTCGCCCGC  AACCTGAACA  GCCACAAAGA
651  AGCCCTGCAA  CTGATGGTCG  AAGCGGCCGA  AGCCGCCGGC  TACAAGGCGG
701  GCGAAGACGT  ATTATTCGCA  TTGGACTGCG  CGTCCAGCGA  GTTCTACAAA
751  GACGGCAAA  ACCACTTGG  AGCCGAAGGC  CGCTCCTACA  CCAACGCGGA
801  ATTTGCCGAA  TACTTGGAG  GCTTGGTTAA  CGAATTCCCG  ATTATTCCA
851  TTGAAGACGG  GATGGACGAA  AACGACTGGG  AAGGTGGGAA  ACTGTGACC
901  GAAAAATTGG  GCAAAAAAGT  TCAATTGGTC  GCGCAGCACT  TGTTCGTAAC
951  CAATCCGAAA  ATTCTTGCCG  AAGGCATCGA  AAAAGGCGTA  GCAAACGCAT
1001  TGCTGTGCAA  AGTCAACCAA  ATCGGTACTT  TAAGCGAAAC  CCTGAAAGCC
1051  GTCGATCTGG  CAAAATGCAA  CCGCTACGCC  AGCGTGATGA  GCCACCGCTC
1101  CGGCGAAACC  GAAGACAGTA  CCATTGCCGA  CTTGGCAGTC  GCCACCAACT
1151  GTATGCAGAT  TAAACCGGT  TCTTTGAGCC  GTTCCGACCG  CATGGCGAAA
1201  TACAACCAAC  TGCTGCGTAT  CGAGGAAGAA  TTGGCGGAAG  CCGCTACTA
1251  CCCCAGCAAA  GCCGCAATTCT  ACCAACTGGG  CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAL TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGACG GCGACAAATC CCGTTATTCC GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGATTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNAL TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVLQV GDDLFTVNP K ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRYG					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRYG					
	10	20	30	40	50	60
	70					
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
	70	80	90	100	110	120
	130					
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNVIINGGEHANNSLNIQEFMIMPVGAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDSKGFPTTV	GDGEGFAPNL	NSHKEALQ	LMVEATEA	AAGYKAGEDVLFA
g652-1	CGAEIFHALKKL	CDSKGFPTTV	GDGEGFAPNL	NSHKEALQ	LMVEAAEA	AAGYKAGEDVLFA
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEY	LEGLVNE	FPIISIEDGMDENDWEGWKLLT
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTN	AEFAEY	LEGLVNE	FPIISIEDGMDENDWEGWKLLT
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGRVQL	VGGDDL	FVTNPK	ILAE	GIEKGV	ANALLVKVNQIGTLSETLKA
g652-1	EKLGGRVQL	VGGDDL	FVTNPK	ILAE	GIEKGV	ANALLVKVNQIGTLSETLKA
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVM	SHRSGE	TEDSTI	ADLAV	TNCMQI	KTGSLSRSDRM
g652-1	SVM	SHRSGE	TEDSTI	ADLAV	TNCMQI	KTGSLSRSDRM
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AAGGCGGCGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCGCCGGA AGCGTTGCCG TCGGGTCCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCCGAC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTGC AGGCGACCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGGCCGA TATCTGGAAG GCCTGGTCAA CGAGTTCGCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAAGT CCAACTCGTT GCGCAGCACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGCGCTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAA GCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES GVMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRVLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIEQFMIMPV GAKSFREALR CGAEIFHALK KLCDKSGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKVLV GDDLFTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGE EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMEVGAKSFREARL
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMEVGAKSFREARL
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLF
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLF
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKKX
a652-1      AAFYQLGKKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgccg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTT TGTtgacggT GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaactgTGC TTTTCGGTGC GCCGGAaagc atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGTc GCAGAaatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAPPMRME VTYGFSGSFG MAFLLTVMCA LPKAASALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNS AMTAALITC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTT TGTGACGGT GATGTGCGCT TTGCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCCGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWLSRHKIT PPRGPRRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
g653	MAAEPMRMPEVTYGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
g653	MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX					
g653	SWLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATSPAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGCGCGCGG AACGATGCG GATGCCGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCCGG ATGCGGTTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCCGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWLSRHKIT PPRGPRRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
a653	MAAEPMRMPEVTKGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
a653	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX					
a653	SWLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX					

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```

g656.seq
1  ATGCCGCGTT TCTCCGGTTC GATTCTCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TCAACACAGc ctTCGACGTT GGAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTCGGGGCG
401 AGGAACCGAC GATGTGAAA TCGCCGAAAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```

g656.pep
1  MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```

m656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCCG TAACTTTGAC
201 TTCGCCGTT TTAATGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCCG
301 TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTTTCGCG TCGGACGAGG ATTCGGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```

m656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLRSRTR ISGEEPTMWK SPKS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	: : : : : : : : : :					
g656	MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPsFKQPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSIINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	: : : : : : : : : :					
g656	ILSVTLTSPVLLMRPTSLRPKSIITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
	: : : : : : : : :					
g656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT  GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGTT TACTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTGCG CGCTAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTGGC
151 GACCGCCATT TGTGCGCGCC GTTGTACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGG TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACAG GCGGCGTGGA TTGCGTTTTG GAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CTTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcC ATCGTCcccG CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GGCACAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGGAC ACACATGAAT TGCTCGTCAA
801 TGAACCGGCC CGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGAGCA CAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAC CGCACAGAAA
1051 GGTCCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAFFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADELDYVGV

251 LAVEMFVVGD THELLVNETA PRTHNSGHH T IDACAAQDQF QQVRIMCNLP
301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAKQ
351 GRKMGHFTVL TTDSDTAFOE AKKLHOSL*

m657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTTGGCA	TCTCTCGCGG
51	CGGACAATTA	GGCAGAAATG	TTACCGTTGC	CGCCAAAACC	ATGGGCTACA
101	AAGTAAACCG	TCTGCACCCC	GATCCGGGAC	CGCCCGGCAC	AGAATTTTGCC
151	GACCGCCATT	TGTGCGCGCC	GTTTAAACAG	CAAGCTGCTT	TGGACGAATT
201	GGCAAAATGC	GCGGCGGTGA	CCACTGAATT	TGAAAACGTC	AATGCCGATG
251	CGATGCGCTT	TTTGGCAAAA	CATACCAATG	TTTCCCCTAG	CGGCGATTGT
301	GTGGCGATTG	CACAAAACCG	CATTCAGGAA	AAGCGATTGA	TACGCAAAAGC
351	GGGATTGCAA	ACCGCGCCGT	ATCAAGTGGT	TTGTAAGGCT	GAAGACATCA
401	CTGAAGCAAG	CGCGCAATTT	TTGCCCGGTA	TCTGAAAAAC	GGCTACGTTG
451	GGCTACGACG	GCAAAGGTCA	AATCCGCGTA	AAAACATTGG	ATGAACCTCA
501	AGCCGCGTTT	GCCGAAACAG	GCGGCGTGGA	TTGCGTTTTG	GA AAAAATGG
551	TGGATTTCGC	CAGTGAATTT	TCCGTAATCG	TATGCCGTTT	GAACAATGAC
601	AACGTGCAAA	CTTTCGACCC	TGCCGAAAAC	ATCCACGAAA	ACGGCATCTT
651	GGCTTATTCC	ATCGTCCCCG	CGCGACTGAG	TGCCACGCTG	CAGCAACAGG
701	CGCGGCAGAT	GGCGCAACGC	TTGGCGGACG	AATTGGATTA	TGTTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCCGTGAC	ACCGATGAAT	TGGTCGTCAA
801	CGAAATCGCC	CCGCGCCCCG	ACAATTCCGG	ACACCATACG	ATAGATGCCT
851	GCGCAGCAGA	CAGTTCCAG	CAGCAGGTAC	GCATTATGTG	CAACCTGCCG
901	CCTGCCGATA	CCAAATTACT	GAGTTCTTGC	TGTATGGCAA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGCTG	CCCTTGCAAA
1001	GCCATCCGAA	TGCACACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAATA	TGGGCACTTT	TACCGTTTTA	ACCACCGATT	CGGACACCCG
1101	ATTTTCAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

m657.pcp

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA
51	DRHLCAQNRD	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLO	TAPYQVVCKA	EDITESAQF	LPGILKTATL
151	GYDGGKQIRV	KTLDLKAFAF	AEHGGVDVCL	EKMVDLRSEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQMAQR	LADEL DYGVV
251	LAVEMFVVG D	THELVVNEIA	PRPHNSGHTH	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSSC	CMANILGDVW	QDGGEGPDWL	PLQSHPNAHL	HLYGKKTAAH
351	GRKMGHFTVL	TTDSDTAFQE	AKKLHSL*		

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60	
m657.pep	MKNISLSP	AMLGILGGGQLGR	MFTVA	AKTMGYKVTVL	DPDPD	APAAEFADRHL	CAPFND
	:: :						
g657	MNTPPIL	PPAMLGILGGGQLGR	MF	AVAAKTMGYKVTVL	DPDPN	APAAEFADRHL	CAPFDD
	10	20	30	40	50	60	
	70	80	90	100	110	120	
m657.pep	QAALDE	LAKCAAVTTEF	ENVNADAMR	FLAKHTNV	SPSGDCV	AI	AQNRIQEKAWIRKAGLQ
	:					:	
g657	RAALDE	LAKCAAVTTEF	ENVNADAMR	SLAKHTNV	SPSGDCV	SI	AQNRIQEKAWIRKAGLQ
	70	80	90	100	110	120	
	130	140	150	160	170	180	
m657.pep	TAPYQV	VCKAEDITEA	SAQFLPGIL	KTATLG	YDGKGQ	IRVKTLD	ELKAAFAEHGGVDCVL
g657	TAPYQV	CKAEDITEA	SAQFLPGIL	KTATLG	YDGKGQ	IRVKTLD	ELKAAFAEHGGVDCVL
	130	140	150	160	170	180	

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQVVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAERTHNSGHHTIDACAADQFQQVVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGVDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGVDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSIX					
g657	TTDSDTAFQEAKKLHQSIX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCGCCCGGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAAATGT TACTGTGTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGCTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTACAGAAA ACGGTATCCT
651 CGCTACTCC ATCGTCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTCOA
801 CGAAATCGCG CCGCGTCCGC ACAATTCGGG CCACCATAAC GTCGACGCCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CAAATTTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCGGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSFSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVG
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSIX*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKTVLDP DPAPAAEFADRHLCAFPND					

a657	MKNISLSPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN	10	20	30	40	50	60
m657.pep	QAALDELAQCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
a657	QTALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ	70	80	90	100	110	120
m657.pep	TAPYQVVCKAEDITEASAQFLPGILKTATLGVDGKGQIRVKTLDLKAFAEHGGVDCVL	130	140	150	160	170	180
a657	TAPYQAICKAEDITEESIQFLPGILKTATLGVDGKGQIRVKTVDLKAFAEHRGVDCVL	130	140	150	160	170	180
m657.pep	EKMVDLRSEISIVVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR	190	200	210	220	230	240
a657	EKMVDLRGEISIVVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR	190	200	210	220	230	240
m657.pep	LADELQYVGVAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP	250	260	270	280	290	300
a657	LADELNYVGVAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP	250	260	270	280	290	300
m657.pep	PADTKLLSSCCMANILGVDVQEDGGEPDWLPQSHPNALHLHYGKKTAAHKGRKMGHFTVL	310	320	330	340	350	360
a657	PADTKLLSSCCMANILGVDVQEDGGEPDWFPQSRPDALHLHYGKKTAAHKGRKMGHFTIL	310	320	330	340	350	360
m657.pep	TTDSDTAFQEAKKLHQSLX	370	379				
a657	STDSDTAFQEAKKLHQSLX	370					

g658.seq

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

g658 . pep

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRRLPRLLLH
51 VGTQPRGDDG ISQDAVEVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVVAQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVIGID
201 VFKFGRNRRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1 ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CCGCATACGA TTACGGAAAT TTCCTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGGA CCTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CCGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTT CAATCCCGCT TTGCGTATCC
501 ATGCTTTTTC CTGAATGCGG TTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAAG CGCATCGCAT CCGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGCGTCGGC AAATTCTGCT
701 GCCGCGCGGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGCT
751 TTTGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LAHLPRLLLH
51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVVAQ RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRLG QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHSAX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
g658	MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLLHVGTQPRGDDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGGVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
g658	ISQDAVFVDVFGGVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFVQRF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVVAQRSRFQDAGQKLRACFSDFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
g658	ADLTFVVAQRSRFQDAGQKLRACFSNVFGLANRLIRRLGQACFAYPRFFLNAVLCNGHA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRRAFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG					
g658	VAAGGNVGM LQRAHRVIGIDVFKFGRNRRRAFCQFVQRPVVKRRAQMAVGKFRRRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFSGNGKHSAX					

1050

g658 :|||||:|||||
 IENGYFVAHGFGNGKHSAX
 250 260

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

a658.seq
 1 ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
 51 CATGCGTGTC GCCGACAACA AACATTTCTA CCGCCAATAC GCCGACGTAG
 101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
 151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
 201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTTCAGA
 251 CGGCATACGA TAACGGAAAT TTCGCCGCGC AAGTCCACCA TTTTTCCTAA
 301 AACGCAATCC ACGCGCGCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
 351 CCGTTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGTTT
 401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
 451 TTTGCAAAAT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC
 501 ATGCCTTTTC CTGAATGCGG TTTTGCSCGA TGGCAACGCA GTCGCCGCTG
 551 GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC
 601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAA TCTTCCAAAG
 651 CGGTTTGTT GTCAAACGCG GCACACAAAT GGCGGTCGGC AAATCCCGCT
 701 GCCGGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
 751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep
 1 MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLRLLLN
 51 VGTQSGWDDG VGEDTVFVNV FGRIEHLVV IVQTAYDNGN FAAQVHHFFQ
 101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
 151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID
 201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRRVG IEYGYFVAHG
 251 FGSNSKHSAX*

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLVGTQSRGDDG					
a658	: : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDNGNFTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
a658	::: : : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVAVQSRFQDAGQKLRACFSDFSLTNHLIRRLGQSRFAYPCLFNAVLCNRHT					
a658	: : : : : : : ::					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRQMAVGKFCRRVRIG					
a658	: : : : : : : : : : :					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFGGNGKHSAX					
a658	: : :					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

g661.seq
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT GCGGACAAAC CCTTCGCGCG CCTCTGTCGG GCGTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
 151 ACCGGAAGAAA CCctgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
 201 TGCCGTGCAG ATTGCCGGCA GCGACCCcga acaGATGGCG Gatgcggcgc
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
 301 cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
 351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGcg
 401 TACCCGTAC cctCAAACc cgtTtgggtt ggcacgacga cgatcaaac
 451 ctgcCcgccg tcgcaaaat cgccgaagat tgcggcattg ccgccCttgc
 501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
 601 CGGCGACATC actTCgcccgc AAAAAGCCGC GcgcgTCCTC AAACAAACCG
 651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
 701 TTCCGCGATT TGAAGCATT TCCGAACAC GGCGTTTAC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCATATC CGCGCCATGC
 801 ACGCGTTTTA TGGTGAAGAC GTCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGCGAAAT GCCCGACGGC GAACAGGCGC GGCCTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
 201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
 251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTGAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq
 1 ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51 GGCGGGCATT ACCGACAAAC CGTTCGCGCG ACTTTGCCGA GATTTTGGCG
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
 151 ACTAGAAAAA CCTTGACCCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCCGCG
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
 351 CGAGCCGCTG GTTGCAGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
 401 TACCCGTAC CCTCAAACCG CGTTTGGGTT GGCACGACGA CCATCAAAC
 451 CTGCCCGTCA TCGCCAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
 501 CGTCC.AC GG ACGCAGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
 551 GAACATCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
 601 CGGCGACATT ACTTCGCGCG AAAAAGCCCA AGCCGTCTC AAACAAACCG
 651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
 701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
 751 GAGTTTGGCA GAATGCGCGG CCGCTATTTT GAACCATATC CGCGCCATAC
 801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
 851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
 201 RRYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFEL CRTRCFACL
 251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWDDHQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPREFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPREFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGGGGCATT ACCGACAAAC CGTTCGCGCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTGACACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTAC CCTCAAACCC CGTTTGGGTT GGCACGACGA CCATCAAAC
451 CTGCCCCGTC TCGCCAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAATGT ACAAAGCGCA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGCA GAATGTACCG CCACTATTTT GAACCATATC CGAGCCATGC
801 ACGCGTTTTC CGGCGACACC GCCGTGTGTC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPREFETL RRTRCFACLA
251 EFGMRMYRHY EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*
  
```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFETL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPREFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRDTSTX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRDTSTX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCCGAC GCAACAATTC GGTTTTGTG
601 GATTTTTCG GCATtcagaC GGCAACGATT ACCGGCTTGA GCCGATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTA TCGAAGAACG
801 CGTGCCGCGA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNNNSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVTLQ FYPWKSFFS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTGAAACA

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1054

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201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCGCGATCAG GATTTCGGAC GCAACGATTC GGTTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCTG CTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCCTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGT GCTGCACAAG CGTTTTTAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVT LH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK					
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK					
m663.pep	70	80	90	100	110	120
	RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYLDDALAAGEKVIILYPHFT					
g663	70	80	90	100	110	120
	RKTVLKQHFKHMAKLMLEYGLYWYASAKCLKSLVRYRNKHLYLDDALAAGEKVIILYPHFT					
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVT LH					
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVT LQ					
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	250	260	270	280	290	
	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.ssq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAAGT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTGGCA

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1055

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151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCCG CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTGTC
601 GATTTCTTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTCCGAGT
751 GAAGATGCCG AGGCCGACGC GCAGCGCATG AACCGTTTA TCGAGGAACG
801 CGTGC CGCAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PV READNTVTLH FYPAWESFPP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

          10      20      30      40      50      60
m663.pep  MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK
a663      MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFPEWDGKK
          10      20      30      40      50      60

          70      80      90      100     110     120
m663.pep  RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
a663      RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
          70      80      90      100     110     120

          130     140     150     160     170     180
m663.pep  AFEMAVYALNQDIPISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
a663      AFEMAVYALNQDIPISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
          130     140     150     160     170     180

          190     200     210     220     230     240
m663.pep  SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH
a663      SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVTLH
          190     200     210     220     230     240

          250     260     270     280     290
m663.pep  FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663      FYPAWESFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
          250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAAGC GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGACgg gGCGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTGGGGGAA CTGGTCTGG CCGCAGCAGG GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAT TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCaa
451 cCgaagcgc gtttcgtcCc acttcacgc gtTTTTTCAA cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTCG GTGGGTGAAA ACTCGATTTT

```

g664.pwp

m664.seq

m664.pcp

a664.seq

1 GTGATACATC CGCACCACCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TATCGGGCGG GCGCACCGG ATGTGCGGTG
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGCG GGATGTTTTC
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAATAA TCTTGGTCCG

1057

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201 GGAACACGGT CAACCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTCGTCCC ACTTCATTGC GTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAG ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF  FINGHGV EIV  HLLISGGAHR MCGRTCVFGE  LVLAQQADV F
51  DTAHGAAGAV  AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFF	INGHGV EIVHLLI	AGGAHRMGR	ACVFGELVLA	QQADV F	DAHGAAGAV
a664	VIHPHHFRAFF	INGHGV EIVHLLI	SGGAHRMCG	RTCVFGE L	VLAQQADV	FDTAHGAAGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHG	QPFLQRKLEP	VAAAGYAVAR	PVVEILVSD	HGFD AFEI	GIGGGAAV
a664	AGKFLVAEHG	QPFLQRKLEP	VAAAGHAVAR	PVVEIFVSD	HGFD AFKI	GIGGGTAVG
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVTTLVFH	RAHIEIAHGD	DDHENIQVVF	QTEARFVPF	HRVEXTIP	RQSRPWACPL
a664	VKDVTTLVFH	RTHIEIAHGD	DDHENIQVVF	QTEARFVPL	HCVFXAIP	RQSRPWACPL
	130	140	150	160	170	180
m664.pep	TRFX					
a664	TRFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGgG acgaaacgcg cttcgGgttg GAAtatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTGGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCGTGC GCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCAAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGC GGAT GTATCATACC CTGCTCGCGC AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCAacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCAAGTTC CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCAT AAACAAACCG
701 TGCCGCCAC GCCGATATG GCGGACAAAC AGCCGATGAT GATTTCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGT TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACG TTTACAGTGC TGGGAAGCCG

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1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTCGGGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGCTGTCG GCGCCTtctgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTTATCGGCT CAAGccgcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTGAGCCGC AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cccGCaggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFIMV AVGDFNMGAM ENKGLNIFNT KEVLADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPTPDM ADKQPMMPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDL LLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDQAA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNMH HEWGILSAVN GNESDTRNCL
501 LAQFADKFS D DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTGCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCACTTCG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCAC GCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGCTGCGC CACGCTGCGC

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYMTVYEK
151 GAENVVRYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPTPDM TDKQPMPIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLTE AEQTFLEGV TEAVVPSLLR
301 GFSAPVHLYN PYSDDDL LLAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLDNAFKA LLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNMH HEWGILSAVN GNESTDRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNOF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMN NFYMTVYEKGAENVVRYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPASYEEMN NFYMTVYEKGAENVVRYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMPIPVKVGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQTFLEGVTEAVVPSLLR					
g665	ADKQPMPIPVKVGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLL	LAHDSADFT	WEAAQTL	YRR	AVANLAT	SDGVELPKHEK
	:	:	:	:	:	:
g665	GFSAPVYLNYPYSDDDLLL	LAHDSADFT	CWEAAQTL	YRR	AVANLAALS	DGIGL
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLL	NAFKALL	LGVPSE	AELWD	GAE	NIDPLRYHQAREALLDTLAVHFLP
	:	:	:	:	:	:
g665	LLAAVEKVISDDLL	NAFKALL	LGVPSE	AELWD	GTENIDPLRYHQAREALLDTLAVRFLP	
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQ	SYEYSPEA	AGWRTL	LRNVCRA	FVLRADPAH	ETVAEKYGE
	:	:	:	:	:	:
g665	KWHELDRQAAKQENQ	SYEYSPET	ADWRTL	LRNVCRA	FVLRADPAH	ETVAEKYGE
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESD	TRNLLAQ	FADKFS	DDALVMD	KYFALVG	SSRRSDTLQQV
	:	:	:	:	:	:
g665	HEWGILSAVNGNESD	TRNCLLAQ	FADKFS	DDALVMD	KYFALIG	SSRRSDTLQQV
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLNPNKARSLIG	SFSRNVPH	FHAEDG	SGYRFI	ADKVIEID	RFPQVAARLVQAFNL
	:	:	:	:	:	:
g665	PKFSLNPNKARSLIG	SFSRNVPH	FHAQDG	SGYRFI	ADKVIEID	RFPQVAARLVQAFNL
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQ	ALQ	RIRAEGL	SKDVGEIVG	KILD	X
	:	:	:	:	:	:
g665	CNKLEPHRKNLVKQ	ELQ	CIRAEGL	SKDVGEIVG	KILG	X
	610	620	630			

a665.seq

1	ATGAAGTGGG	ACGAAACGCG	CTTCGGTTTG	GAATACGACT	TGATATTTT
51	CATGGTCGTC	GCCGTGGGCG	ATTTCAATAT	GGGTGCGATG	GAAAAACAAGG
101	GTTTGAACAT	CTTTAACACC	AAGTTCGTCC	TTGCCGACAG	CCGTACCGCC
151	ACCGATACCG	ATTTTGAAGG	CATCGAATCC	GTGGTCGGAG	ACGAATATTT
201	CCACAACCTG	ACGGCGAACG	GGGTGACCTG	CCGCGACTGG	TTCCAGCTTT
251	CGCTGAAGGA	AGGGTTGACC	GTGTTCCGCG	ACCAAGAAAT	TTCCGGCGAC
301	CGCGCCAGCG	GCGCGGTGCG	CGGTATCGAA	AACATCCGCC	TGCTGCGCCA
351	GCACCACTTC	CCCGAAGACG	CAGGTCGCGC	CGCACATCCG	GTGCGCCCGG
401	CCCGATATGA	GGAGATGAAC	AATTTCTACA	CCATGACCGT	TTATGAAAAA
451	GGCGCGGAAG	TGGTGCGGAT	GTATCACACC	TTGCTCGGGG	AAGAGGGGCTT
501	CCAAAAAGGT	ATGAAGCTCT	ATTTCCAACG	CCACGACGGA	CAGGCTGTTA
551	CCTGCGACGA	TTTCCGCGTG	GGCATGGTGG	ACGCGAACGG	CATCAACCTC
601	GACCAATTCG	CTTGTGGSTA	GACCCAAGCA	GGTAGCGCCG	TTTTAGATAGC
651	TCAAGGGCGT	CCTGAAAAAC	ATGTGTTCSA	GTTAACCATC	AAACAACCGG
701	TGCCGCCCAC	GCCCGATATG	GCGGACAAAC	AGCCGATGCT	GATTCCCGTC
751	AAAATCGGGG	TGCTGAACCT	CAACGCGGAA	GCGGTGGCAT	TTGATTATCA
801	GGGCAAAACG	GCGAACGAAG	CCGTGTTGCT	GCTGACCGAA	GCCGACAAGA
851	CTTTCAGATT	GCAAGGCGTA	ACCGAAGCCG	TCGTTCCCTC	GCTGCTGCGC
901	GGGTTCAGCG	GCGCGGTGCA	TCTGAACTAT	CCGTACAGCG	ACGACGACCT
951	GCTGCTTCTG	CTCGCCCATG	ACAGCGACGC	CTTACGCGCG	TGGGAAGCCG
1001	CACAAACGCT	CTACGCCCGT	GCCGTCGCGC	CCAACCTTGC	CGCGCTTTCA
1051	GACGCGCTCG	ATTGTCCGAA	ACACGAAAAA	CTGCTTGCCG	CCGTCGAAAA
1101	AGTCATTTCA	GACGACCTCT	TAGACACAAGC	TTTCAAAGCC	TCGCTTTTGG
1151	GTGTGCCGTC	TGAAGCCGAG	CTGTGGGACG	GCGCGGAAAA	CATCGACCCG
1201	CTGCGCTACC	ATCAGGCGCG	CGAAGCCTTG	TTGATATATC	TTGCCGTCGG
1251	CTTTCTCCCG	AAATGGGCAG	AATTGAACCG	TACGGCGGCG	AAGCAGGAAA
1301	ACCAAAAGTA	GAGATACAGC	CCCGAAGCCG	CCGGTTGGCG	CACGCTGCGC
1351	AATGTCTGCC	GCGCCTTCGT	CCTGCGCGCC	GATCCCGGCG	ACATCGAAAA

1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTC AAC GCGAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCGCCCGGCC TGGTGACGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

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a665.pep
1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMIPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDLLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DLLLONAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNROAA KOENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLNPKN
551 ARSLIGSFSS NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

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m665/a665 97.3% identity in 638 aa overlap

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m665.pep      10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRATDTDFEGIES
|||||
a665          10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRATDTDFEGIES

m665.pep      70      80      90      100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
|||||
a665          70      80      90      100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF

m665.pep     130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG
|||||
a665         130     140     150     160     170     180
PEDAGPTAHPVRPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFQRHDG

m665.pep     190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
|||||
a665         190     200     210     220     230     240
QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPDM

m665.pep     250     260     270     280     290     300
TDKQPMIPVKVGLLNRNGEAVAFDYQGKRATEAVLLLEAEQTFLLLEGVTEAVVPSLLR
:|||||
a665         250     260     270     280     290     300
ADKQPMIPVKIGLLNCNGEAVAFDYQGKRATEAVLLLEAEQTFQFESVTEAVVPSLLR

m665.pep     310     320     330     340     350     360
GFSAPVHLNYPYSDDLLLLL LAHDSDAFTRWEAAQTLYRR AAVANLATLSDGVELPKHEK
|||||
a665         310     320     330     340     350     360
GFSAPVHLNYPYSDDLLLLL LAHDSDAFTRWEAAQTLYRR AAVANLAALS DGVELPKHEK

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1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNFAKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCATTGA ACCGAAGTGC ATTTGACAT  TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCGA GGGCGGGCGA GCCGCTGGTG
151 TTGACGGTTC CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGCG
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACAACAA
301 TCGCTGATGG GGTGTATGTC TTCCGGCGGC AATCTGTTTA CCCAGTGCAG
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG AAAAAAAGC CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCGC
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGTAACCG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGCAAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGCGACCGC GCCGCGCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCGCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAGAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGGC ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCCGA AGGCCGTCTG
1351 AAAAACAAATG TTTTCGAGTT AACCATTAAC CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA GTCGGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAATATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACATG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GCGCGCGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCGCAC CCGCGGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCTGTCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCCTT
2251 ATCGGCTCAA GCCGCGCGAG CGACACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGTCCGCG GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGGGCGG
2551 CAGGAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGCGA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

m665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLSLV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKRRYPV
151 LLSNGNKIDG GEFSGRHWV KWEDPFAKPS YLFALVAGDL AVTEDREFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YLDLIFMVVA
251 VGFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR AGRARRRIEN IRLLRNQFP
351 EDAGPTAHVP RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMIPVK VGLLNNGEA VAFDYQKKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLELL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAKAL LLGVPSEAEI WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROQAAK QENQSYEYSP ETADWRTLRLN VCRAFLVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDDL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

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1 ATGAGCAAAA CCGTGCATTA TCTCAAGAC TATCAACGC CCGCTACCA
51 TATTCTCAAA ACCGATTAC ATTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGAGA GGGTAGGGGA GCCGCTGGTG
151 TTGACCGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTT TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAACACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTTTGA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC ACAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTT CAAACCGAGC TATCTGTTTG
551 CTTTGGTCGC GGGCGATTTG GCGGTAACGG AAGACTATT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CCGGATGGAA AACAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCT CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCTGCG TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CCCCCCGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCGGA AGGTCTGCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ACTATCAGGG CAAACGCGCG

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1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CCGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AACGCTCTA
1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GGCGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTGCGCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCC GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCCGG
2051 CCTTTGTCTT GCGCGCGGAC CCGCGCGACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTG
2201 CCGCAAGATT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC
2251 GTCGGCTCAA GCCGCGCAG CGACACCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCGAGCTT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGTACCGCTT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTR FVLADSRTAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQFP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYKAG AEVVRMYHTL LGEQFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPPTPDMT DKQPMIPVK VGLLNNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLEPKHEKL LAAEKVIDS
601 DLLDNFAKAL LLGVPSEAEL WDAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL ALQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QQVRLAQHP KFSLENPNKA RSLIGSFSRN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVG EIVGKILD*

m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVRYLKD	YQTPAYRILE	TELHFDIAEP	QTVVKSRLTV	EPQRAGEPLV	LDGSAKLLSV
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAD	VPSERFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFAKPS
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
g665-1	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
	250	260	270	280	290	300
m665-1.pep	YDLDFMVVAV	GDENMGAMEN	KGLNIFNTR	KFVLADSRTA	DTDFEGIESV	VGHEYFHNWT
g665-1	YDLDFMVVAV	GDENMGAMEN	KGLNIFNTR	KFVLADSRTA	DTDFEGIESV	VGHEYFHNWT

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMMPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMMPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRVAANLATLSDGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRVAANLAALSDGIGLPGHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFAKALLGVPSAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1	DLLDNAFAKALLGVPSAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTLQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRIAQEGLSKDVGEIVGKILD					
g665-1	VKQELQCIRIAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

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1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTGATAT TAACGAACCG CAACCATTTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG CGGTGGCGGC
201 GGATTATGTG TTGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

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1066

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501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCCGGC TTGCGCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCCGC
1001 CCGTGGCGCG TATCGAAAAC ATCCGCCTGC TGGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GTCCGACCGC ACATCCGGTG CGCCCGCCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATT
1251 CCGCGCGCGC ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAAACAAAT TGTTCGAGT AACCATCAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA ATCGGGCTGC
1451 TGAATGCAA CGGCGAAGCG GTGGCATTG ATTATCAGGG CAAACCGCGC
1501 ACCGAAGCCG TGTGTGCTGT GACCGAAGCC GAACAGACCT TCCAGTTTCA
1551 AAGCGTAACC GAAGCCGTGC TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCCGTGCC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAAATG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAACAT CGACCCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTT CCGTCCGCTT TCTGCCGAAA
1951 TGGCACGAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGC GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCGCAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACCGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTC
2251 GTCGGCTCAA GCGCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAAATC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTTCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGCGA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pap

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1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDOEFSGDR ASRAVRRIEN IRLRQHQPFP
351 EDAGPTAHPV RPARYEEMNN FYTMTVYKGG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAGQRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAETRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRL VCRAFLVLRAD PAHIETVAEK
701 YAEAMQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QOVQTAHQHP KFSLENPNKA RSLIGSFSRN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVG EIVGKILD*

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a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pap	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGSAKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGSAKLLSV
	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDTRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YLDLIFMVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTPPTPDMAKQPMIPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLELLLAHDSDAFTWEAAQTLYRRVAANLAALSDGVELPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLGVPSEAEIWDGAENIDPLRYHQAREALLDILAVRFLPKWHELNRAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPAAAGWRTLNRVCRAFVLRADPAHIETVAEKYAEQAQNMTHWGLSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

		790	800	810	820	830	840
		850	860				
a665-1.pep	V	KQALQ	RIRAQ	EGLSK	DVGEI	VGKILD	X
m665-1	V	KQALQ	RIRAQ	EGLSK	DVGEI	VGKILD	X
		850	860				

g666.seq

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1 ATGCTTTGTA TGAATTATCA ATCAAACCTCA GCGAAGGAG TGCTTGTAGC
51 TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGTACGGCGG TAGCGTGTGA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA
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g666.pep

1	MLCMNYQSNS	GEGVLVAKTY	<u>LLTALIMSMV</u>	ISGCQVIHAN	OQKVNTNSAV
51	IAGADAHTPE	HVTGLTEQKQ	VIAADFVYAS	ANPLATQAGY	DILKQGGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGAFFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLEKDGX	PLKFMEAVVA	RXXRLLSLN*		

m666.seq

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1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51 TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTC AAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCGTGA CATTGCAACGG GACTGACCGA
201 ACAAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGGCTTG GCGCGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AACATTGAC CACATTGAT GGGCGTGAGA CGGCACCCAT GCGTGCCAGC
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
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m666.pep

1	MFCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGVNTHSAV
51	ITGDAHTPE	HATGLTEPGK	VIASEFMVNS	ANPLATQAGY	DILKQGSAA
101	DAMVAQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTFD	GRETAPMRAT
151	PELFLDKDGO	PLKFMEAVVV	VARVWRLLSL	N*	

m666/g666 93.9% identity in 181 aa overlap

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      10      20      30      40      50      60
m666.pep  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g666      MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTHSAVIAGADAHTPE
          10      20      30      40      50      60

      70      80      90     100     110     120
m666.pep  HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGSSAADAMVAVQTTLSLVEPOSSGL

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a666.seq

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1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51 TAAAACATAT TTATGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAAGTCAT CCATGCCAAT CAAGGTAAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGCTG CAGACGCTCA CACGCGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGCGGG TAGCGCTGCA
301 GATCGCATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGGCAGC
451 CCGGAATTAT TTTTGATAAA AGATGGTCAA CATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
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a666.pep
  1  MPCMNHQSNs  GEGVLAKTY  LLTALIMSMT  ISGQCVIHAN  QGKVNTHSaV
51  ITGDAHTPE  HATGLTEQK  VIASDFMVS  ANPLATOAGY  DILKQGGsAA
101 DAMVAVQTTL  SLVPEQSSGL  GGGAFVLYWD  NTAKTLTTFD  GRETAPMRAT
151 PELFLDKDGQ  PLKFMEAVV  VARVWRLLSL  N*
```

	10	20	30	40	50	60
m666.pep	MPCMNHQSN	GEGVLAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VTGADAHTPE
a666						
	10	20	30	40	50	60
	MPCMNHQSN	GEGVLAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VTGADAHTPE
	70	80	90	100	110	120
m666.pep	HATGLTEQ	KQVIASDFM	VASANPLAT	QAGYDILK	QGGSAADAM	VAVQTTL
a666						
	70	80	90	100	110	120
	HATGLTEQ	KQVIASDFM	VASANPLAT	QAGYDILK	QGGSAADAM	VAVQTTL
	130	140	150	160	170	180
m666.pep	GGGAFVLY	WDNTAKTL	TTTFDGR	ETAPMRAT	PELFLDK	QGQPLKF
a666						
	130	140	150	160	170	180
	GGGAFVLY	WDNTAKTL	TTTFDGR	ETAPMRAT	PELFLDK	QGQPLKF

```
m666.pep      NX
               ||
a666           NX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAattgcg
151 GAtttccttc agcgtgcccc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgccagC
251 GGCACATTcg ccctcggetG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCGTATCCC AATAGCGCGC GGC GTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTCT
651 GCTGCGCGAA CAGCACCCT TCGTCATCCG GCAGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGA V MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMLVLP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHFEVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATCCGC ATCCGTTTGA
51  TTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCTTTC AGCCTGCCCC TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCAG CTGCCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTT CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCGC CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHPIAR GVDVYQGA V MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHNL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```
m667.pep      10      20      30      40      50      60
MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
||:  | |::  | ||:||||: |||||:| | : :||| | | | | | |
```

```

g667      MRFVFCLGGEIVSDPCDFHLVVFVRVESAAADQTTETQIHQIRIHGIGFAIIADFLQRARVER
              10          20          30          40          50          60
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAVAE
              70          80          90          100         110         120
g667      FPHFAAVHTQLARKAAQFRHIVQRHIRPRLVKREQIHQIAVALVITADVVPLEIAAVAE
              70          80          90          100         110         120
m667.pep  IAVAHIPiARGVDVAVYQGAVMqYQGQIETAaAVPTDQLRRMFfNQFEKfSNDHfLAVIHLAD
              130         140         150         160         170         180
g667      IAVARIPiARGVDVAVYQGAVMqYQGQVETAaAVPADQLRRMFfNQFEKLGNHdfFAIVHLAD
              130         140         150         160         170         180
m667.pep  GADMYFILPpTHAARNRHNLmKMLLHKIAARLSTaFVLGNQHHL
              190         200         210         220
g667      GADMNLVLPpAHTAGNRHNLMEVVLHKIAAGLCAaFLLRQHHfVIRQGRrQVIQRtDTL
              190         200         210         220         230         240
g667      HIGYGFNIeSQNRiHGStLHsKTDLRLLCHX
              250         260         270

```

a667.seq

```
1 ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTTCCATTTC GTATTTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGCTT ATTTACCAGCA TCGGTTTTCG AATAATTGCG
151 GATTTCCTTC AGCCTGCGCG CCGTGAACGC CTTCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTCT CCCTCGGCTG GTAAGCGCG AGCAATCCA TCAATCGCA
301 ATGACGTTGG TGGTAGCGGC TGATGTAGTT GTTCCAATTG AAATCGCGGC
351 TGTCCGCGAA ATCGCGCTGC CCCATATCCC AATAGCGCGC GGCCTTGATG
401 CCGTGTAGCA GCGAACGGTA GTCAGAAACC GCGAGGTGCA AACCCCGGCC
451 GTTCCAACCT ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CATTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACTCG
601 ATGAAGATGA TGCTGCATAA AATCCCAACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACCCTT TCATCGTCGG GCGAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TTAATAA.CAG ACTTGCGCCT
801 ATTTGTTCAT TAA
```

a667.pap

1	MRFVFCFLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVVAAADV	VPLEIAAAVE	IAVAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNL
201	MKMMHLKPII	RLSTAFLLGK	QHHFIVGQRG	RQVIQRTDTL	HIGYGFNIEN
251	QNRGHDSTLY	LKXDLRLLC	*		

```

      10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPFDHFVVRIQPAADQTETQVHQISVCRVGFALADFLQPARMEC
a667      ||: |::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      10      20      30      40      50      60
      MRFVCLGGELVSDPLDFHFVFCVESAADQTETQIHQIGIYRIGFALADFLQPARVER
      70      80      90      100     110     120
m667.pep  LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAVAE
a667      ||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      LPHLAAVHTQLARKTAQFRHIVQRHVRPRLVKREIQIHQIAMTLVVAADVVPLEIAVAE

```

		70	80	90	100	110	120
		130	140	150	160	170	180
m667.pep		IAVAHIPIARGVD	AVYQGAVM	QYQGIETA	AAVPTD	QLRRMFFN	QFEKFSNDHFLAVIHLAD
a667		IAVAHIPIARGVD	AVXQRTVM	QNRQVETA	AAVPTD	QLRRMFFN	QLEKFGDNHFLAVIHLAD
		130	140	150	160	170	180
		190	200	210	220		
m667.pep		GADMYFILP	PTHAARNR	HNLMKMML	HKIIAARL	STAFVLGN	QHHL
		:					
a667		CTDMDFILP	PTHAARNR	HNLMKMML	HKIPTRL	STAFLLGK	QHFFIVGQRGRQVIQRTDTL
		190	200	210	220	230	240
a667		HIGYGFN	IESQNR	GHDSTLY	LKXDLRL	LCHX	
		250	260	270			

```
g669.seq
  1  ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
    51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCTTTGGGC
   101  GGAACGTCCT CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
   151  GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TCAATCTCTC
   201  CAACAGGCCA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAACACGG
   251  CAACCTTCAA AGACAGATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
   301  GAGATCAAAC GCATCTGTA A
```

g669.pep
1 MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLLRQHG
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```
m669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAATTT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCTTTGGGC
101 GGAACGCTCC CCATCATCAT GACAGACGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCTCT
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAGACCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTCAATGCC
301 GACATCAAAC GGATACTGTA A
```

m669.pep
1 MRRRIKKHQF INAPHIVLEI RIMKLHRAVF FLGRKRPHHH DSSLRRQHG
51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKF PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAPHIVLEIRIMKLRHAFVFLGRKRPHHHDSLLRQHGIEGMGDFDKQI					
	: : : : : : : : :					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLRHAFVFLGRKRPHHHDRSLRQHGIEGMGDFDKQI					
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1   ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTCC  CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT  CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1   MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGI EGMGFDFKQI
             |||||:|||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1   ATGACTTGTT GCAGGAAGTCT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CCGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CTTTTCCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1   MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCWC
101 PPESWEGKAS FLCASEPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1   ATGACCTGTT GCAGGAAGTCT CTTGGCGCGT TCGTGTTCG GGTGGTAAA
51  AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CCGTTCGTCA AACAAACATTA

```

1074

```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
g670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep    FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
g670         FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep    SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              |||||
g670         SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
1  ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGGTAA
51  AAACGCTTCC GCGTTCGT CTTGAGGAT TTGCCCTTA TCACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCGGACCAT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51  IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
a670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```



```

              70          80          90          100          110          120
m670.pep      FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
|||||
a670          FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              70          80          90          100          110          120

              130          140          150
m670.pep      SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
|||||
a670          SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
              130          140          150

```

g671.seq

```
1 ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51 GCCCAAAATG CGGTGGCAA AGCCAGAGCC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCCAT GACGACAACGG
151 GAAATGAATG ACAGAgccaa TGCAAACAgg cggggtTGGa ACgaggCAAA
201 GGCAGGTCg gccaaggGTG CGGCaaAGAG TTTggcaaaa AAGaagggAAA
251 ccaccCATGC cACCATCgaa ccTGTTCcG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCCGC GATCAGCGcg gAGGCGAGGA GGTcGGCAAT
351 GGGGAGGCTA TTCATTcGTt ACATGCGCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA
```

g671.pep

1	MISRVTIKTP	FNAPNTPPKM	RLAKRPRTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
101	EMTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

m671.seq

1	ATGACCAGCA	GGGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACGCC
51	GCCCAAAATG	CGGT'TGGCAA	AGCCCAAAAC	GACCGCGGAA	ACTGCGCTGG
101	TACGACGCGA	ACGGAGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
151	GAAATGAACG	ACAGAGCCAA	TGCAAAACAG	CGGGGT'TGGA	ACGAGGCCAA
201	GGCGAGGTCG	GCGAAGGAGG	CGGCAAAGAG	TTTGGCGAAA	AAGAAGGAAA
251	CCACCCATGC	CGCCATTGAG	CCTGCCTCCG	CAATCACGCC	GCGCATCGCG
301	GATACGACGA	TGCAGGCGGC	GATGACGGCG	GAGACAGGGA	GGTCGGCAAT
351	GGGGAGGCTA	TTCAATTGTT	ACGTGACCGG	CGATACCGTG	TACGCGCAAT
401	TTGTTCAAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

```
m671.pep
1  MTSRVTIKTP FNPANTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGR.					

```

g671      |||||:|||||:|:|||||:|||||
          RGWNEAKARSAKGAASLAKKKETTHATIEPASAITPRIVETMQAAMTAEARRSAMGRL
              70          80          90          100          110          120

              130          140          149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          |||||:|||||:|||||
g671      FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
              130          140

```

a671.seq

a671.pap

m671/a671 93.9% identity in 148 aa overlap

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCACGCCG	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCG	CGCCGCTATC	GACATCATTA	AAGCACAATA	AATCGCGCGC
151	GCACTGCCGC	CGTTGTCTAG	CGTTGTCGCC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	CCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CCGCCCTTAT
301	ATTAAAGCCA	TTCTGTGTCA	GACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	CGCCTTCCCC	AACGCTCAGG	CAGTCTGTTT	CGATGCCTAT	CACCCCTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	Ggagctgtt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCtgg	AAAACGCTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATC	CGGTTAA		

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITPEDALYA AHAGADALGL VFYPQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAEFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCGGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAATC GGTTCGATGA TCCGGCGGTG
551 TGGAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLLEAY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAEFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICG	ITPEDAAAA	AAAGADAVGL	VFFQGSSRAV	DIARAKKITA	ALPPFVSVVA
g672	10	20	30	40	50	60
	MRKIRTKICG	ITPEDALYA	AHAGADALGL	VFYPQSPRAI	DIIKAQKIAA	ALPPFVSVVA
m672.pep	70	80	90	100	110	120
	LFVNESQNIR	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRF
g672	70	80	90	100	110	120
	LFVNESQNIR	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRF
m672.pep	130	140	150	160	170	180
	DAQALLFDAY	HPSEYGGTGN	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	130	140	150	160	170	180
	NAQALLFDAY	HPSEYGGTGH	RFDWTLLEAY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
m672.pep	190	200	209			
	SGGVEASKGK	KDAAKVAEFI	ATANRLSRX			
g672	190	200				
	SGGVEASKGK	KDKPAKVAEFI	ATANRLSRX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCTGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

a672.pep

```

1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRF DPQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICGITTTPEDAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA					
a672	MRKIRTKICGITTTPEDALYA AHAGADALGLVFYPQSPRAVDI IKAQKITAALPPFVSVVA					
	10	20	30	40	50	60
m672.pep	70	80	90	100	110	120
	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF					
a672	LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRF					
	70	80	90	100	110	120
m672.pep	130	140	150	160	170	180
	DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
a672	DAQALLFDAYHPSEYGGTGH RFDWTLAEYSGKPWVLAGGLTPENVDEAIRITGAEAVDV					
	130	140	150	160	170	180
m672.pep	190	200	209			
	SGGVEASKGKKDAAKVAEFIATANRLSRX					
a672	SGGVEASKGKDPKVAEFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

g673.seq

```

1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCCGCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTGTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGCGGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

```

1079

```

651 GGGCGAGGAG CTGCCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEDA AAEVSAKHG LRIANLLELL KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGTAAG CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEDA AAEVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDH RNALNDRLNQ NVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||||

```

1080

```
g673      YTDDTAQFVFVDTPGFQTDHRNALNDRNLQNVTALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEGDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVSGWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```
a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGCGGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG
```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```
a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDPGFQTDH RNALNDRNLQ NVTEALGGVD
101 VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVEM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF D TKVFLKVWVK VKSGWADDIR
301 FLRELGL*
```

m673/a673 99.7% identity in 307 aa overlap

```
           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60
```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYF
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAEE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	:					
g674	YIQKIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq
 1 ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTGCGGTAC AAGCCGTTTA
 51 CCAATCCCTT ATCAACCGCA CCGCCGCCCG CGAGATTGCT AAAACATCC
 101 GCGAAATGCC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAAACTT
 151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TACATCCGAC AAATCCGCCC
 201 CCTGCTCGAC CGCGACGAAA AAGACCTCAA CCCATCGAA CGCGCCGTCC
 251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAC GCCCTACCCC
 301 GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG CGGCACGGA
 351 CGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
 401 GTCCCGACGA GCCCAAACGC CGTTGA

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep	1	MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL				
	51	FFGTQTNAEE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP				
	101	VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*				
m674/a674	99.3% identity in 141 aa overlap					
	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAEE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLDREKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1 ATGAACACCA TCGCCCCaa cctcgacgGC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAa catcaccgtc
151 gccACCGTAC CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGCTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEM LKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAACAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGCTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGCGT
 151 GTTCAAAACC ACTTCGTCGC CTTGCGCGCG TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGACG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCGCGCA ACAGACCGAC
 301 GGTGCGCCG AAAAATACTT GGTGCGTCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
 451 GTCGCCGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYSEFIWETV RLCRFRRHSR SVDFDVFDRK DFNFLTAFR
 51 VQNHVAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
 101 GRAEKYLVR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGCGT
 151 GTTCAAAACC ACTTCGTCGC CTTGCGCGCG TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGATG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
 301 CGTCGCGCCG AAAACACTT GGTGCGTCG TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG
 451 GTCGCCGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYSEFIWETA RLCRFRRHSR SVDFDVFDRK DFNFLTPFR

1086

51 VQNHFAVAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAVAFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLT	AFRRVQNHFAVAFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKYLVRGFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq
 1 ATGCCGCGAGA TTTTGGTGCG GATTTTCCTC ATTCCGGTATT CCTTTATTTG
 51 GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTCAATT TCCTCAGCCG CTTCGGGCGT
 151 GTTTAAACCC ACTTCGTCGC CTTACGCGCG TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
 301 GGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCAA
 351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCGGTAAAGG TAGTCGCGGT TTTGCTGCGG
 451 GTCGCGGTTG CCTGCGCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep
 1 MPQILVRIFL IRYFSIWETA RLCRFRHRSR SVDFDVFDRK DFNFLTFFRR
 51 V*NHFAVAFR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
 101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHTAF AVKVVAVFAA
 151 VAVACRPVDD LDDFGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAVAFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLT	PFRRVXNHFAVAFR				
	10	20	30	40	50	60
	70	80	90	100	110	120

1087

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
          |||
a677      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTDRRAEKHLVGRFAQFGINDDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFVDQLIKLVFQCL
          ::|||
a677      GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFINQLIKLVFQCL
          130     140     150     160     170     180

          190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
          |||
a677      PSGGRNVVFGFGTHIVCGX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51  CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTggCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTcATTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACCGGC GCAGTTTCGG CGGTcGGTCT GGGCTTTGCC
301 AACCGcATTT TGGCGGGTGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFO PRLFALALSF ISLEVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCcGCTGT TTGCATTGGC
201 TCTGTcGTTc ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACcAGC GCAGTTTCGG CGGTcGGTTT GGGCTTTGCC
301 AACCGcATTT TGGCGGGCGT ATTCGGTGCA TTGAAAGCGC TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51  FADLAFASFO PRLFALALSF ISLEVIACLI QKMLRSLTGS AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	: : : : : :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : : :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : : :					
g678	IMLASKTDLPDTEEWQSYTVFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCGCG CCAAACCTCT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTCG ATCGTTCCAA CCCCCTCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CCGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	: : : : : :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	: : : : : :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	: : : : : :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTGT TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCAGGACT ATTTCCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTTCA TGTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTAAAtg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

g680.pep

```

1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

m680.seq

```

1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GCGGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CCGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GGCAGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCTG
451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCAGGACT ATTTCCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

m680.pep

```

1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFECFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPENK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90      100     110     120
m680.pep TLCLVLQNTMTWFIKSTISRSSRLRFKXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      TLCLVLQKTITWFIKSTISRSSRLRFKXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC
          70      80      90      100     110     120

          130     140     150     160     170     180
m680.pep ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFECFTW

```

```

g680      |||||
          ASLRIGAEKVAEKSRVWRWGSICMLRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180
          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSLMTPPKRTVCRSGRFLMX
          190      200      210      220

```

a680.seq

1	ATGACGAAGG	GCAGTTCGGC	AATATCCAGC	CCCCGCGCGG	CGATATCGGT
51	GGCGACGAGG	ACGCGCAGGT	TGCCGCTCTT	GAAGGCGTTG	AGTGTTTTCGA
101	CGCGCGCTTG	TTGGGAACGG	TGCGCGTGT	TGCGCTGTGC	GGACAGGTTG
151	CGGCGCACCA	GTTGCGCGCT	TACGCGGTCG	ACGCTTTTGT	TGTTTTTGC
201	GAACACGATG	ACCTGGTTCA	TATGCAAATC	GACAATCAGC	CGTTCGAGCA
251	GGTTCGCGTT	CTGAATGGTA	TCGACGCGCA	TGATGTGCTG	CTCGACGTTG
301	GCGTTGGTGG	TGCTTGGCGC	GGCGACTTCG	ACGGTTTTCG	GCGCGTTTAT
351	GAAGTCTTGC	GCCAGTTTGC	GTATCGGGGC	GGAGAAGGTG	GCGGAAAAGA
401	GCAGGGTTTG	CGGTGGGCGG	GGCAGCATCT	GCATGATTTT	GCGGATGTCTG
451	TCGATAAAAC	CCATATCCAG	CATACGGTCG	GCTTCGTCCA	AAACGACGAT
501	TTCGACTTTG	TTCAAATGGA	TGTTTTCTG	TTTCAGTGG	TGCAGACGCC
551	GTCCGACGGT	GGCGACGACG	ATTTCGCAGC	CGGCACGCAG	GTCGGCGGTC
601	TGTTTGTCCA	TATTCATACC	GCCGAACAAG	ACGGTGTGGC	GCAGCGGCAG
651	GTGTTTGATG	TAG			

a680.pep

1	MTKGSSAIISS	PRAAISVATR	TRRLPSLKA	SVSSRLCWER	SPCIACADRL
51	RRTSSRVTRS	TLCLVLQNTM	TWFIKCSKIS	RSRRRLF*MV	STAMMCOSTL
101	ALVVSCAATS	TVSGAFMKSC	ASLRIGAEEKV	AEKSRVWVRW	GSICMILRMS
151	SIKPISSIRS	ASKTKTISTL	FKWMEFFCFTW	SSSRPTVATT	ISQPARRSAV
201	CLSIFFPNPK	TVSWRSGRFLM	*		

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMS VATRTRRLPSLKALSVSSRLCWERSPC IACADRLRTSSRVTRS					
a680	: : : : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m680.pep	TLC LVLQNTMTW FICKSTISRSSLRF XFMVSTAMMCC STLALVVFCAATST VSGAFMKSC					
a680	: : : : : : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m680.pep	ASLRIGAEKVAEKSR VWWRGSI CMILRMSSI KPISSIR SASSKT TISTLFKW MFFCFTW					
a680	: : : : : : : : : : : :					
	130	140	150	160	170	180
	190	200	210	220		
m680.pep	SSSRPTVATTISQPARRSA VLCSIFIP PNKTV WRSGRFLMX					
a680	: : : : : : : : : : : :					
	190	200	210	220		

g681.seq
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCCAA
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacgq

1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCGgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCCCGCGT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTTDMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNLEEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VEVGFVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTTCG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GATCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTTDMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VEVGLVAAEE TPAAVVFKNG GFAVEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

m681.pep      10      20      30      40      50      60
               MTTDMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
g681          MTTDMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
               10      20      30      40      50      60

```

1092

```

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG DGLECAVFGKLPCAA
          |||||
g681      KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG NGLECAVFGKLPRAA
          70      80      90      100      110      120

      130      140      150      160      170      180
m681.pep  FGLGEQCGGFRVGFVG DVEADDAEVVRIVGVFVGLVAAEETPAAVVFKN GGFAVEEADGP
          |||||
g681      FGLGKQCGGFRVGFVG DVEADDAEVVGVGVFVGLVAAEETPAAVVFKN GGFVAVKEADGP
          130      140      150      160      170      180

      190      200      210      220      230      239
m681.pep  VLF G DGVGGDTAVECRGKCLCKCVHYGNTLGX-KLT DFTTIRALSADGGGLV VQCAFFAA
          |||||
g681      VLF G DGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIP ALSADGGGLV VQCAFFAA
          190      200      210      220      230      240

      240      250      260
m681.pep  LRCFCIFGVWKRIRAVFCGRRX
          |||||
g681      LRCFCIFGVWKRIRAVFCGRRX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGGAAC TTGCGGATT
651 TACCACGATT CTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVFGDIGEA DDAEVVRVVG
151 VVGLVAAEE TPAAVVFKN GFAVEEADGL VLF G DGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAFFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

```

      10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          :
a681      ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          10      20      30      40      50      60

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG DGLECAVFGKLPCAA
          |||||
a681      KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA
          70      80      90      100      110      120

```

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	NTLGXKLTDFTT	IRALSADGGGLV	VQCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKVHCG	NTXGGKLADFTT	ILALSADGGGLV	VQCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGCTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. ..EMAMPSEP DWIQTAFMA YGFIRFPTDR
101 PIRTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          |||:|||| |: ||||| |||:|| ||||| ||||| ||||| ||||| |||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPTGFR
          ||||| |: ||||| ||||| ||||| ||||| ||||| ||||| |||||
g682      PILILIDYICVNDEIKMPSEPDWIQTAFCMA-GFIRFPTDRPILTRQSGVVRISPTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          ||||| ||||| ||||| |||||
g682      YPTRSLPKSKKAYGX
          120     130

```

a682.seq

```
1 ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51 GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA
```

```
a682.pap
1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLN STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYK*
```

```

m682.pep      10      20      30      40      50      60
MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEFFCLITPDLTMHYC
|||||
a682          10      20      30      40      50      60
MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEFFCLITPDLTMHYC

m682.pep      70      80      90      100     110     120
PILILIDYEMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
|||||:|
a682          70      80      90      100
PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS

m682.pep      130
LPKSKKAYGX
|||||
a682          110
LPKSKKAYGX

```

g683.seq

1	ATGATTAAGG	AAACCCTAAT	GCGCCCAATC	TTCCTATCTT	TCGTTTTACT
51	CCCTATTTTG	ATRACCGCCT	GCAGACACCC	GGACAAGTGT	GCCCGATGGG
101	AAAATATCGG	CACAATCTCA	AACGGCAATA	TTCATACATA	TATTAAATAA
151	GACAGTGTGA	GAAAAACGG	AAATCTGATG	ATTTTCCAAG	ATAAAAAAGT
201	TGTTACCAAT	CTGAAACAAG	AACGTTTTGC	CAACACCCCC	GCATACAAGA
251	CTGCCATTGC	CGAGTGGGAA	ATCCATCGCA	ACAACAACAA	ATACCGCTTA
301	AGTTCGCTAC	AGGATTATTG	TACAAAAAAC	ACGGAAATTT	CCACACAAAA
351	CTACACAGCC	TC TTCCTCC	GCCCGATGAG	CATCCTGTCC	GGGACATTAA

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

m683.pep
1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISILS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..
1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTACCAAT CTAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..
1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130 140					
m683.pep	SSLRPMISILSGLTLEKQYETVCGKKLX					
g683	SSLRPMISILSGLTLEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

m683.seq
1 ATGATTAAGG AAACCCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTACCAAT CTAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

m683.pep
1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
a683      |||||
      10      20      30      40      50      60
m683.pep  IFQDKKVVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
a683      |||||
      70      80      90      100     110     120
m683.pep  IFQDKKVVVTLNKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
a683      |||||
      70      80      90      100     110     120
m683.pep  IFQDKKVVVTLNKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
a683      |||||
      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
a683      |||||
      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
a683      |||||
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

```

g684.seq
1  ATGCGCCTTT TCCCATCGC CGCGGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

```

g684.pep
1  MRLFPIAAL TLAACGTQVS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGGVLYQT DPYRINTAQN HVWADTLDDM LEAALSNAFN RLDSTRTFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTAAL QGLKQAAQOM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

```

m684.seq
1  ATGCGCCTTT TCCGATTGC CGCGGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CAGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

```

m684.pep
1  MRLFPIAAL SLAACGTQVS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGGVLYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTERK TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

Homology with a predicted ORF from *N. gonorrhoeae*

m684/g684 97.7% identity in 172 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFFPIAAALSLAACGT	VQSTQYFVLPDSRYIRPAT	QGGETAVEVRLAEPLKRGGLVYQT			
a684	MRLFFPIAAALTLAACGT	VQSTQYFVLPDSRYIRPAT	QGGETAVEVRLAEPLKRGGLVYQT			
	10	20	30	40	50	60
m684.pep	DPYRLNTAQNHHVWADT	LDDMLEAALSNAFNRLD	STRIFVPASRSGSTEKWT	VYIDAFOGS		
a684	DPYRLNTAQNHHVWADT	LDDMLEAALSNAFNRLD	STRIFVPASRSGSTEKWT	VYIDAFOGS		
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHHVWADT	LDDMLEAALSNAFNRLD	STRIFVPASRSGSTEKWT	VYIDAFOGS		
a684	DPYRLNTAQNHHVWADT	LDDMLEAALSNAFNRLD	STRIFVPASRSGSTEKWT	VYIDAFOGS		
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQQGDGYAAMTAALEQGLKQAAQMVEX
              |||||||||||||||||||||||||||||||||||||||||||||||||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQQGDGYAAMTAALEQGLKQAAQMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1   TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCct GCGCCGTCTT GCCGGCCGCC
151 TGTTTCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGCGCATG
251 CCGTTGTGCC GAAGAATCCC GAACgctcg ccgtgtAcga CtgggCGGCG
301 TtggatACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTGTC AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGC GAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCAATTA CCGCGGGGCC GGTGCGGAA CCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCC CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CCGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAST PVATLTVPPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLTEPGVN VGATTAPVRV DYLPAPFKA ATVTGLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKRGGLVLS VTGNKVSFAFG TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIQGEPPAA
301 VEVLDNALVC GTNAWKRRQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1   TTGTTTTGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTTCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCC
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCAGAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAAGG CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGCG CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCTT GCCGCGAAT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGCG GGAGCAGTTG AAGCGGCGCT TAAAAAGGC AGAACCCTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep


```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
g685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT

m685.pep      70      80      90      100     110
VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685          70      80      90      100     110     120
VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV

m685.pep     120     130     140     150     160     170
DYLQPAFDKAATVGTILFEPDYEALHRYNPQLVITGGPGAEEYQLAKNATTIDLTVDNGN
g685         120     130     140     150     160     170     180
DYLQPAFDKAATVGTILFEPDCESLHRHNPQFVITGGPGAEEYQLAKNATTIDLTVDNGN

m685.pep     180     190     200     210     220     230
IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGF
g685         180     190     200     210     220     230     240
IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAGF

m685.pep     240     250     260     270     280     290
TQSLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
g685         240     250     260     270     280     290     300
TQSLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA

m685.pep     300     310     320     330     340     350
VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAAGKKX
g685         300     310     320     330     340     350
VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTATAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTGCGCCG AACCTGCCGC CGAAAAAAT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTCAGC CCTGCATTG ACAAGCGCGC AACGGTGGGG ACGCTGTTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATTACC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGGAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGCGCG AGATTGACGC GCTGTTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
 901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAGCGCA AGCAAATCAT
 951 CGTCATGCCT GCCGCGAACT ACATTGTGCG GGGCGGCTCG CGGCAGTTGA
 1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
 1051 GCGGCGGGGA AAGAGTAG

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

a685.pep
 1 LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
 51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
 101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
 151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
 201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSFAFGTQSR LASWIHGDIG
 251 LPPVDESLRN EGHGQPVSE FYKEKNPDWI FIIDRTAAIG QEGPAAVEVL
 301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFKAEPV
 351 AAGKE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

m685.pep	10	20	30	40	50	60
	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSP					
a685	10	20	30	40	50	60
	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSP					
m685.pep	70	80	90	100	110	120
	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	70	80	90	100	110	120
	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
m685.pep	130	140	150	160	170	180
	PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS					
a685	130	140	150	160	170	180
	PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQ LAKNATTIDLTVDNGNIRTS					
m685.pep	190	200	210	220	230	240
	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGK RGLVLSVTGNKVSFAFGTQSR					
a685	190	200	210	220	230	240
	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGK RGLVLSVTGNKVSFAFGTQSR					
m685.pep	250	260	270	280	290	300
	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	250	260	270	280	290	300
	LASWIHGDIGLPPVDESLRNEGHGQPVSEFYKEKNPDWIFIIDRTAAIGQEGPAAVEVL					
m685.pep	310	320	330	340	350	
	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEFVAAGKKX					
a685	310	320	330	340	350	
	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFKAEPVAAGKEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)
 1 ..AATTTCCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
 151 ATTGTGGAAG CCGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
 201 GGTGAGGCG GATATTTTGG CCAACGCCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

g686.pep (partial)
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFSG GIAAALWPFVI
 101 AVGGMVVFVS PMDAVKAESV NGTGFVRIG M*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
 151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
 201 CGCGTTTGAA TCCGTGCGCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
 301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
 401 TCGGCGGGAT GGTGTTGCTA TCCGTCCCAA TGGATCCGGT AAAGGCTAAA
 451 TCCGTCACG GGAATACCG CTTCATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep
 1 MLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
 101 EADILGNAFY VVAVYIPRAF SGGIAAALWP VIAVGGMVFV SVPMDAVKAK
 151 SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGF	GGGIARSVQLG	
m686	LKKFVLGGIAALVLAACG	GSEGGSGAXX	XXNFSCSADD	VFNDICSAVEGF	GGGIARSVQLG	
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAG	IVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFSG			
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFSG				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPFVIAVGGMVFVS	VPMDAVKAESVNGTGFVRIGMX			
m686		GIAAALWPFVIAVGGMVFVS	VPMDAVKAESVNGTGFVRIGMX			
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)
 1 ..AATTTCCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 51 TGAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
 101 GTGGCGCGTT TGAATCCGTC CCCTACTCCT TCGCTCAGCA TACTACCGGT
 151 ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTGCGTCA
 201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
 301 GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

      10      20      30      40      50      60
m686.pep  LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686      NFSCRADDVFDDICSAVESFGGIARSVQLG
                        10      20      30

      70      80      90      100     110     120
m686.pep  AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686      AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                        40      50      60      70      80      90

      130     140     150     160
m686.pep  GIAAALWPVIAVGGMVFSVPMDAVKAKSVNGTTGFIIRIGMX
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a686      GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIIRIGMX
                        100     110     120     130

```

g687.sag

```
1 ATGAAATCCA GACACCTCGC CCTCGCCCTC GGCGTTGCCG CCTGTGTCGC
51 CTTTGCCGCG TGCACACGCA AAGTCCA AAC CAGCGTCCCC CGGCACAGCG
101 CGCCTGCCGC TTGCGCAGCC GCGCGCCCCG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACACGACG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTCG CGCCGCTTcg
251 AACCTGTTTT GAGCAACACG GCCAAGTCTT TTAAGACGA TATGTACCTG
301 CGTACCGACA ACGTGCTGCT GCAGAAAGAA ATGCTGCCCG TGGCACGCct
351 cGCCGCCGCG CTGATATGCG CTGCCGCCGA AAGCAAAGAT TGGGCGAACA
401 GCCATATTTT CGATGCCGAT GTCAACCAAA AATCAAGCT GCAAGAGCGC
451 GAAGTCTCTCA AAAAAATGGCT GGGCGAACAA ACcgcttTfG ACGGCAAAAA
501 AGTCTTGTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCCAAACC TTCCAAATCG ACGGTACGCC CACGGTATTC
601 GTCGGCGGCA AATATAAAGT CGAATTGGC GACTGGGAG CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG
```

g687.pep

1	<u>MKS</u> <u>RH</u> <u>LAL</u> <u>AL</u>	<u>GVA</u> <u>AL</u> <u>FAL</u> <u>AA</u>	CDSK	QVTSVP	ADS	AAPA	SLVEG
51	NYTV	LANPIP	QOQ	AGKEVL	EFF	GYFC	PH
101	RTEH	VVWQKE	MLPL	ARLAAA	VDMA	AAESKD	VANS
151	EVL	KKWLGE	Q	TAFD	GKKVLA	AYESP	ESQAR
201	VGG	KYKVEFA	DWES	GKNVLD	LLADK	VREEQ	KAAQ*

```
m87.seq
1      ATGAAATCCA  GACACCTTGC  CCTCgGCGTT  GCCGCCCTGT  TCGCCCTTGC
51     CGCGTGGCAG  AGCAAAGTCC  AAACCAGCGT  CCCCGCCGAC  AGCGCGCCGT
101    CCGCTTCGCG  AGCCGCCGCC  CCGCGCAGGG  TGGTCGAAGG  CGAAAACTAT
151    ACCGCTCTTG  CCAACCCGAT  TCCCCACAG  CAGGCAGGCA  AAGTCGAAGT
201    CCTTGAAGTT  TCTGGCTATT  TCTGTCCGCA  CTGCGCCCA  CTCGAACCTG
251    TTTTAAAGAA  ACACGCCAAG  TCTTTTAAAG  ACGATATGTA  CCTCGCTACC
301    GAACACGTCG  TCTGGCAGAA  AGAAATGCTG  ACGCTGGCAC  GCGTCGCCGC
351    CGCCGCTCGAT  ATGGCTCGCG  CGCACAGTCA  AGATGTGGCG  AACAGCCATA
401    TTTTTCGATG  GATGGTCAAC  CAAAATAACA  AGCTGCAAAA  TCCGGAACTG
451    CTCAAAAAAT  GGCTGGGCGA  ACAAACCGCC  TTTGACGGCA  AAAAAGTCCT
```

```

501 TGCCGCTAC GAGTCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687  97.0% identity in 234 aa overlap

              10      20      30      40      50
m687.pep    MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              |||||
g687         MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              10      20      30      40      50      60

              60      70      80      90      100     110
m687.pep    QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEVWQKEMLTLARLAAA
              |||||
g687         QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEVWQKEMLPLARLAAA
              70      80      90      100     110     120

              120     130     140     150     160     170
m687.pep    VDMAAADSKDVANSHIFDAMVNVQIKLQNEVLLKKWLGEQTAFDGKKVLAAYESPESQAR
              |||||
g687         VDMAAADSKDVANSHIFDAMVNVQIKLQNEVLLKKWLGEQTAFDGKKVLAAYESPESQAR
              130     140     150     160     170     180

              180     190     200     210     220     230
m687.pep    ADKMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              |
g687         AGKMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCAGC AGCAAAGTCC AAACCAAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTGACGGCA AAAAACTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRHLALGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
a687						
	10	20	30	40	50	60
	MKSKHLALGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMTLARLAAAVD					
a687						
	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMTLARLAAAVD					
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687						
	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
m687.pep	190	200	210	220	230	
	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687						
	190	200	210	220	230	
	KMQLTETTFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGACACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	CGCTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTRNGII
101	KERSNLTIVYF	ENGVLVRTEG	DALQNAAEAL	RAKQNAADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGACACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	CGCTGCAGTG
101	CCGAACGCGT	TTCACGTGTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAAACATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTRNGII
101	KERSNLTIVYF	ENGVLVRTEG	DVLQNAAEAL	KDRQNTDKP*	

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688    90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRAVAA
              |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g688          VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFPPSYKLKIIQGNELEPRAVAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :|||  :|||  :|||  :|||
g688          DALQNAAEALRAKQNAKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51  AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCCG CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51  NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLTIVYF ENGVLVRTEG NALQNAAEAL RVKQNAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688    93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRAVAA
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a688          VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRAVAS
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTIVYFENGVLVRTEG
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKDRSNLTIVYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :|||  :|||  :|||  :|||
a688          NALQNAAEALRVKQNAKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g589.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCCTAC CTGCCCGCGA
101 TTCCCGAAAT GCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcgatgg tgcgcgattTA TTATTCGGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTG TGATGGTTGT GCCGCTGGCC
451 GCACCATAGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GCGGGGCGAT
501 TTTTCGTTTT ttggcGgcgt ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTGTCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTTCAGG CATTACAGTT CGGTTTCGATG TTCGCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGTGTC ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CGCGTTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTCC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCC
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAAAGGAA ACGAAAAAAA CGGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

g689.pep (partial)

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFSTA PQQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRVAQA FGAGMAVVIV GAMVRDYYSG RKAQMFAFI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPLVPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFOAFSFGSM FAFLTSSSFV YRQLYHVTPH
251 RYAWVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCCT GTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCCGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATAGCGGAA AAAGTATGCG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGCTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGCTCC TCAACTGCG CGTCGTGCAG GCATTCCGGT CCGGCATGAC
501 TGTGGTCAAT GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTGTCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTGTTGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCGTGCTGTC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCC ATGTTCCGCT
851 TCTGACCGA ATCTTCTTC GTGTACCAGC AGCTCTACCG TGTACGCCCT
901 CATCAATACG CTTGGGCGTT TGCATCAAC ATCATCACGA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAACCT GTCCCAACTC
1051 GCGGCCGTGC TGTTTTTTCC GTTGCCCCG TTTTGGCTGC TGGTCCGCTG
1101 CGTGATGTTT TCCGTCCGTA CGCAGGGCTT GGTGCGTGA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGAC GACGGTTCGG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGCG TCTGCTGCGA TCGTGCCTGG

```


m689.pap

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Homology with a predicted ORF from *N. gonorrhoeae*

N. gonorrhoeae:

m689.pcp

g689

m689.pcp

m689.pcp

m689.pcp

m689.per

m689.pap

m689.pap

m689.pcp

9689 LWLCSHKAWKENEKKRIL
390 400

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTCCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AACTGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGCTCA CTGCCCTGCC GTTGGCCGCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGACG GCATTCCGGT GCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGGCGCA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTTCGT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCTT GCCCAAGCCC GCCGTCGGCG GCAAATCGG CAGGATGTG
751 TCCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCGC
801 GATGGGTAT CTGTTTTTTC AGGCATTGAG CTTCCGGTTCG ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCTCAC ATCATCAGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCGT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCGGCCGTCG TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCCGGTGA AACACGCAGG
1151 CGTGTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGCAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTCCGTGG
1351 AAAGAAACG GCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVPASSA
151 EQLNLNRVVQ AFGAGMTVVI VGAMVRDYSY GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGREFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVT
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

m689.pep	10	20	30	40	50	60
a689	10	20	30	40	50	60
m689.pep	70	80	90	100	110	120
a689	70	80	90	100	110	120
m689.pep	130	140	150	160	170	180
a689	130	140	150	160	170	180
m689.pep	190	200	210	220	230	240
a689	190	200	210	220	230	240

9690.seq (partial)

1	ATGAAAACCA	AAACGTCATC	ACTTCCCTTA	TGCGTTGCCG	CAATCATGCT
51	GGCCGCGCGT	TCCCAGAGCA	AAGAAGATAA	AACGAAAGAA	AACCGCGGCA
101	CCGCGCGCTT	GTCTTCGCG	TCATCGGCTT	CTTCCCAAGT	CGATTTCGAA
151	CCGCGCGCAT	CCGCCCCGTA	TAACGTCAAG	CAGGCAGAAA	GCGCGCCACT
201	GTGAAATTGC	ACCCCGCTGC	ACCCCGCCGC	CGGCATTGGC	GATCTCATAC
251	AGCAAATCGC	CGAACACATC	GACTCGGACT	GTCTGTTTGC	CCTTTCCTAT
301	AACGAACTGG	AAACCGGTTT	CGGCTTACCC	GGCGGGCGCT	ATGACAACAT
351	ACAGCGGctG	CTgtttCCCG	ACATCCGCCC	TGAAGATCCC	GACTTACCAT
401	AGAAATCAT	GCTGGCAATC	GAAGACTTGC	GTTACGGAA	CGCACCATC
451	AGcgGCGAGT	CACAAGATGC	CATAATTGGA	CAGGAACGCC	gcctccGaGa
501	agCGACGCTG	ATGCTGACAC	AGGGCACTCA	AAAAACCCGC	GGaCAAGCGG
551	AGGAACCGAA	ACGCGCACGT	TATTTTGAAG	TTTCGGCAAC	ATctcGctat
601	TTgaaccgG	ACAACAacGG	ACTTggcgG	AATTGTTCCA	ACATCGGCCA
651	ATTGCCCGCT	TATCTGAAA	TGCACGGAGA	ATGCTTGAA	AACCAATCAC
701	TCTTCCGGCT	GTCCAACCGT	GAACGCAAT	CCGACAAACC	GTTTTTAGAC
751	ATCCATTTTG	ACGAAATATG	CAAAATCACG	CGTATTGTGC	TTTACGAAA
801	AAATATCTAT	...			

g690.pap (partial)

1	MKNKTSNLVK	WLAAIMLAAR	SPSKEDKTKE	NGASAASSSA	SSASSQTDLQ
51	PAASAPDPNVK	QAESAPL*NC	TGLHPAAGIG	DLIQQIAEHI	SDCLFALSH
101	NELETFRGLP	GGGYDNIQRL	LFPIRDPED	DYHQKIMLAI	EDLRVGTRTI
151	SRQAQDAIME	QERRYLEATL	MLTQGSQKTR	GQGEFPKRAR	YFEVYSATSAY
201	LNRHNNGLGG	NFYQIIGQLP	YLMKHGEMLE	NQSLFRLSNR	ERNPDKPFLD
251	IHFDENGKIT	RIVVYEKNII	...		

m690.seq.

1	ATGAAAAACA	AAACCTCATC	ACTTCTCTTA	TGGCTTACCG	CAATCATGCT
1	GACCGCGTGT	TCTCCGAGCA	AGAGCAGATA	AACCAAGAA	GTCGGTGCAT
101	CCGCTGCTGT	GTCTCCGCGC	TCATCAGCTC	CTTCCCAAAC	CGATTTCGAA
151	CCGACCGCAT	CCGCCCTCGA	TACGCTCAAG	CAGGCAGAAA	CGCGCCGCCG
201	GTCAAAATTG	ACCAGCTGCG	ACCCCGCACT	CGGCATTGAC	GATCTCATGC
251	AGCAAAATCG	CGAACACATT	GACTCGGACT	GTCTGTTTGC	CCTTTCCCAT
301	CACGAATCCG	AAACCCGTTT	CGCGTTACCC	GACGGTGGCT	ATGACAACAT
351	ACAGCGGCTG	CTGTTTCCCG	ACATCCGCCC	TGAAGATCCC	GACTACCATC
401	AGAAAAATCAT	ACTGGCAATT	GAAAGCTTTC	TTTACCGGAA	GCGCAGCATC
451	AGACCGGCAG	CACAAAATGC	CTTAGTGGAA	CAGGAACGCC	CGCTCCGAGA
501	AGCGACGCTG	TTGCTGATAC	AGGGCAGTCA	AGAAACCCGC	GGCAACAGGC

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGA AACAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTACAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAG CGTATTGTCG TTTACGAAA
801 AAACATCTAC TTCATCCAA ACACGGGCGC AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1 MKNKTSLLL WLTAIMLTAC SPSKDDKKE VGASAASSA SSAPSQTDLO
51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI-
151 SRQAQNALME QERRLREATL LLIQGSQETR QGGEPEKPTR YFEVSATPAY
201 SSRHNNLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKPFPLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690 89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep MKNKTSLLLWLTAIMLTACSPSKDDKKEVGASAASSASSAPSQTDLOPTASAPDNVK
g690      ||||| |||:||||: |||:|||| ||||| ||||| |||||:|||||
      10      20      30      40      50      60
m690.pep MKNKTSLLPLWLAAILAARSFSPKEDKTKENGASAASSASSQTDLPASAPDNVK
g690      ||||| |||:||||: |||:|||| ||||| ||||| |||||:|||||

      70      80      90      100     110     120
m690.pep QAESAPPSNCTSLHPATGIDDLMQIAEHI DSDCLFALSHHELETRFGLPDGGYDNIQRL
g690      ||||| |||:||||: |||:|||| ||||| ||||| |||||:|||||
      70      80      90      100     110     120
m690.pep QAESAPLXNCTGLHPAAGIGDLIQIAEHI DSDCLFALSHHELETRFGLPGGGYDNIQRL
g690      ||||| |||:||||: |||:|||| ||||| ||||| |||||:|||||

      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQKIILAI EDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      190     200     210     220     230     240
m690.pep QGGEPEKPTRRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      190     200     210     220     230     240
m690.pep QGGEPEKPRARYFEVSATSAYLNRHNNLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      250     260     270     279
m690.pep ERNPKPFPLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      250     260     270
m690.pep ERNPKPFPLDIHFDENGKITRIVVYEKNIY
g690      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51 GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCCCT GTCCACGGCA TCCGCCGCTT CGTCTTCCGC GCCCCAAACC
151 GATTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCGGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGGC TTACGGAAG
451 CGCACGATCA GCCGCGAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGCGCA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGACA CAACAACGGA CTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTTAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSLLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDFDYHOKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEEP RTRYFEVSAT
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
	MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	QTDLQPTASAPD			
a690	MKNKTSLLLLWLAAMMLTACSPSKEDKTKENGASAASTASAASSAPQTDLQPAASAPD				
	10	20	30	40	50 60
m690.pep	60	70	80	90	100 110
	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
	70	80	90	100	110 120
m690.pep	120	130	140	150	160 170
	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170 180
m690.pep	180	190	200	210	220 230
	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLENQSLFRL				
a690	ETRGQGEPEPKRTRYFEVSATPAYSSRHNNLGGNFQYIGQLPGYLKIHGEMLENQSLFRL				
	190	200	210	220	230 240
m690.pep	240	250	260	270	279
	SNRERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX				
a690	SNRERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTCCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT
 201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGGCGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691>:

g691.pep
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGHNELRK IRAAFKMGD RARLKMVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCGGCTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691  97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep  VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQSQHNELRK
          |||
g691       VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90      100     110     120
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||
g691       IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISSDVFNRNNEARDYVESRYHSSMDFAVDEL
          70      80      90      100     110     120

          130     140
m691.pep  EIQRFFHILTPQQQMWLSCLKX
          |||
g691       EIQRFFHILTPQQQMWLSCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRAAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```
m692.seq
1      GTGTTGCACA  CGCTTTGTCTG  CTGTTTCGGAA  TCGATACGCC  GGATTTCGGCG
51     GAATGCGCAGG  GAATGCGCGGA  TTAAGAGACA  AAAATGCCGT  CTGAACACGG
101    ATACAGTTCA   GACGGCATCA   TTTTATACGA  CTGCCTTATT  TGGCTGCGCC
151    TTCAATTCCAT  CGCGGACAGG  ATTTGTATGCC CTGGAAGCGT  TTGTGCGCGGT
201    AGGCTTTTAA   CGCGTCGGAG  TTTATAGCCT  CGGTACGCT  TTTAAGCCAT
251    TGGCTGTCTT   TGTCTGGCGGT TTTGACGGCA  GACCAGTTGA  CATAGGCCAA
301    GCTCGGTTCT   GTTGACAGGG  CTTCCGTTGAG CTTCATCGCC  CTGCTTATGG
351    CGTAGTTGCC   GTTGACAGCG  GCAAAATCCA  CGTGCGCGCG  GCTACGCGGC
```

m692.pgp

1	VLHTLCRCSE	SIRRIRRNGR	EWRIKQKCR	LNTDTVQTAS	FYTTALFGCA
51	FIPCGRGVFA	LEAFVRVGFSE	RVGVIKLGJV	EKPLAVFVGG	FDGRFPVDIGK
101	ARFLEQGGFQ	LHAAAYGVVA	VDDGKIHWGA	ATRQLRGFKL	DAADFVQVLG
151	DVRFEGCGQRI	DAVEFDDPTQ	FVEHHQDAGE	GVRVVGRGQF	DDFVDFQIRF
201	QLARVQSQR	GRHLEDFGDV	QIVFFFEVIAE	IGFVLEDVDV	QLALSQCQIR
251	AYIVGKLDQF	DGVAFFLLQLG	LDLFFDHIAE	VADGRASDDF	FFRRAVVGGG
301	RSGCCGRAVF	LTAAGGEDER	ECGGKGFEF	GFHTFS*	

Homology with a predicted ORF from *N. gonorrhoeae*

m692/g692 91.1% identity in 338 aa overlap

	10	20	30	40	50	60
m692.pep	VLH	TL	CR	CS	ES	IR
g692	VS	HT	CR	CS	ES	IR
	10	20	30	40	50	60
m692.pep	LEA	FV	RG	FE	RV	GV
g692	LEA	FV	RG	FE	RV	GV
	70	80	90	100	110	120
m692.pep	VDD	GK	IH	VGA	ATR	QL
g692	VDD	GK	IH	VGA	ATR	QL
	130	140	150	160	170	180
m692.pep	VGR	VV	RG	YG	AA	VF
g692	VGR	VV	RG	YG	AA	VF
	190	200	210	220	230	240
m692.pep	QLA	LS	QC	QI	RA	IV
g692	QLA	LS	QC	QI	RA	IV
	250	260	270	280	290	300
m692.pep	GGR	SG	CG	GR	AV	FL
g692	GGR	SG	CG	GR	AV	FL
	310	320	330			
m692.pep	GGR	SG	CG	GR	AV	FL
g692	GGR	SG	CG	GR	AV	FL

a692.seq

1 GTGTTGCACA CGCTTTGTCG CTGTTTCGGAA TCGATACGCC GGATTTCGGCG

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```

51 GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAATTGA CATAGGCAAA
301 GCTCGGTCTT TGAACACAGG CTTCCGGTCAG CTTTCATCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCCTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGCGCG GGTCCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGCTAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC GCGCCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGCGC CGCTATCTTT TTGACCGCCG CAGGCGGCCA
951 GGATGAGCGC GAGTGGCGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRIRNRG EWRKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFPTQ FVEHHQDAGE VGRVVRGYYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFELQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

m692.pep	10	20	30	40	50	60
	VLHTLCRCSESIRRIRNRGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
a692	10	20	30	40	50	60
	VLHTLCRCSESIRRIRNRGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
m692.pep	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLVYFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
a692	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLVYFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAATRLRGFKLDDFDVQV	LGDVRFQCGQRIDAVFEFPTQ	FVEHHQDAGE			
a692	130	140	150	160	170	180
	VDDGKIHVGAATRLRGFKLDDFDVQV	FGNVRFQCGQRIDAVFEFPTQ	FVEHHQDAGE			
m692.pep	190	200	210	220	230	240
	VGRVVRGYYGAAVDFDFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
a692	190	200	210	220	230	240
	VGRVVRGYYGAAVDFDFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
m692.pep	250	260	270	280	290	300
	QLALSQCQIRAHIVGKLDQFDGVAFFL	QLGLDLFFDHIAE	VADGRAEDDF	FFRAVVG		
a692	250	260	270	280	290	300
	QLALSQCQIRAHIVGKLDQFDGVAFFL	QLGLDLFFDHIAE	VADGRAEDDF	FFRAVVG		
m692.pep	310	320	330			
	RSGCGGRAIFLTAAGGEDER	ECGGKGFE	EGFHIFS			
a692						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.sseq
1   TCGGCATTTG TGTGCCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTCGCGGT TGGTCGTGCG ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTTG TCACGACGCG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCGCGT TCCTGTGTGA CCGCCTTCGA TACGCGGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGGCGGC ACTTCCGCGA AGTCTTCGAT AAACACCGCG
851 CTTTTTTCGC GCAGGTGTG CACGACGAAT TTGTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATCTTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCAATC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```
g694.pep (partial)
1   SAFVLPKHFM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAHG
51  FMPPSAYGCG YFPQHFGFRG RACRYADFAP AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDVDF
301 AHINRRAEFF QSTFDNTDCP IHTGAEEARI GKDDGFSVHK FCIPCSBGIH
351 VFLLXLCDGR YQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.sseq
1   TTGTTTCCG CATCCGGCAC ACGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCGGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCCTTCGCGC CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGCGCG TTTGCCGGTT
451 GGTGCTGCGA TAGCAGATAT CTTCCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTGCG GGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCG GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGACGGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCA GCGAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCAGC
1151 CGAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGTROK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
```

```

151 GRIADIFLV RIADIGETRV QRGDVDFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

```

m694/g694      86.8% identity in 372 aa overlap

              10      20      30      40      50
m694.pep      LVSASGRQKCR LKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694           :|||||  '|||||:|||||:|||||:|||||:|||||
              10      20      30      40
              60      70      80      90     100     110
m694.pep      TLAFAYGFVPPSAYGCGYFPHQHFGGRGRACRYADFVFKPCALQVACIIHHIRIDSARC
g694           : |||:|||||:|||||:|||||:|||||: |||: |||: |||: |||: |||: |||
              50      60      70      80      90     100
              120     130     140     150     160     170
m694.pep      RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694           R|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
              110     120     130     140     150     160
              180     190     200     210     220     230
m694.pep      FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
g694           F|||:|||||:|||||:|||||:|||||: |||: |||: |||: |||: |||: |||
              170     180     190     200     210     220
              240     250     260     270     280     290
m694.pep      VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694           V|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
              230     240     250     260     270     280
              300     310     320     330     340     350
m694.pep      TFFTQVVHDEFVNNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694           : |||:|||||:|||||:|||||:|||||:|||||:|||||: |||: |||: |||: |||
              290     300     310     320     330     340
              360     370     380
m694.pep      SFS DGINIFLLGFY GGRCCPTPPT PHRRRX
g694           |||: ||| : || : |||: |||
              350     360     370
g694           PCS DGIHVFLXXLCDGRYCOAPPT PHRRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.mseq
1   TTGGTTTCGG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGTTTCGCC CTGCGGCGCG AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCGGAC TTTGTTTTT CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCGG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCGGTT
451 GGTGCTCGCA TAGCAGATAT CTTCCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCATCTGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG

```

1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGTTGTGCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRRIDIFLV RIADIGETRV QRGDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPFR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1  TTGCTCTCAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCC TCGGCGACGG TTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTTGGAGCA TACGAAAAATA
451 CACCCCTTCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAAACATA TCAAAACGGC
601 AGGTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG CGCGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695 >:

```
g695.pep
1  LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQONSQRF QSKPAERYAD
51  CPHPARRRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPESRTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1  TTGCTCTCAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCC TCGGCGACGG CTTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATCTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTGC
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAAACATA TAAAGCGGC
601 AAGTTTCTG CCGCTGCCTC CTTGTTGAAA GGGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1  LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

m695/g695 90.8% identity in 305 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHRHRQYFAERKGDARSGFRCAAQRRHPQRQFQSKPAERPAHRPHHPARRRR
g695      LPQTRPARRHRHRQYFVERKGDARSGFXCAAQCONSRQFQSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90     100     110     120
m695.pep  LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIYPVPVPTLQDR
g695      FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTMPTQENASDGIYPVPVPTLQDR
      70      80      90     100     110     120

      130     140     150     160     170     180
m695.pep  LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGGSSASA
g695      LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTGGSSASA
      130     140     150     160     170     180

      190     200     210     220     230     240
m695.pep  HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS
g695      HTVETAQNLYNQALKHYQNGRFSAAALLLKGADGGDGGGSIQRSMYLLQLSRARMGNCS
      190     200     210     220     230     240

      250     260     270     280     290     300
m695.pep  VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA
g695      VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA
      250     260     270     280     290     300

m695.pep  AVRKRKX
g695      AVRKRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

```

a695.seq
1  TTGCCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAAATATT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCAGC
101 GTCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGAACG ATACGGCGAT
151 TGTCCCATC ACCCTGCCCG TCGCGGACGG TTTGACCCTG CTTCTGAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251 CCGCCTGTT TCCCCTGTT TCCCGCAATA TTCAGGATAT GCGGCTCGAA
301 CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATCCCTATC CCGTTCCAC
351 TCTGCAAGAC CGTTTGATT ATCTGGAAG CACACTCGT CCGCTGTCGA
401 ACGAAGTGA AACCTTAAAC GGCAAAGTCA AAGCACTGA GCATGCGAAA
451 ACACACCTT CCAGCAGGGC ATACGTCCAA AACTCGAGC ACCGCAAGT
501 GAAAGAGCAT TACCTCAATA CCGAAGGCG CAGCGCATCC GCACATACCG
551 TCGAAACCGC ACAAACCTC TACAATCAG CACTCAAACA CTATAAAAGC
601 GGCAGTTTT CTGCCGCTGC CTCCTGTTG AAAGCGCGG ACGGAGGCGA
651 CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701 CGCGTATGG CAACTGCGAA TCCGTATCG AAATCGGAG GCGTTACGCC
751 AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAAATCGG
801 CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAG GCGACTTGGC
851 GCAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAA ACGCGCCGCC
901 GCAGCCGTGC GAAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

```

a695.pep
1  LPQACPARRH HCHRQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSAACSSPV SRNIQDMRLE
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDDRKLKEH YLNTGGSSAS AHTVETAQNL YNQALKHYKS
201 GRFSAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NRFKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAARKRA
301 AAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

m695/a695 88.3% identity in 308 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:
a696.seq

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTC ATCAGCCGCA GCATCTTTGA
201 CTTGGCTTTT CGCTTCTTC ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTG GCTTCTTTC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

           10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSSFLGTCLC
           |||
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSSFLGTCLC
           10      20      30      40      50      60

           70      80      90      100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
           |||
a696         ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
           70      80      90      100     110     120

m696.pep    X
           |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTGCCCGG
51  ATTTTTATC CGTGTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTTCG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACCGGC GGGGCATCCG
501 GCTGTCGGTT TGGTTTATAT TGTCTCTCT TTCAGGCGGG CTGCTGTTT
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTC GGATGCGGCG
751 GTGGGGTTCG GCGGCGGAC CAGTATGGAT TTCACATTG CCGTAATTCA
801 GGGTGC GGCGG GGTTTGGAAG TCGTGCCGCT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTC CACGCTGGG
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSIMTLFSV LVPFMAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRGRILSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```


1123

201 GFGWYLSLGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVVFSTLG
 301 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq
 1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
 51 ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTGT GATAAGGTGC
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG
 151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
 251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGCGGTTTCG
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
 351 TGCATTCCGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAGCGCGG
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA
 451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
 501 GTTGTGCGTC TGGTTTATGC TTTCACTCTT TCGGGGCGG CTGCTGTTT
 551 CCGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
 601 GGCTTCGGTT GGTATCCCT CTGGGTTTGT GTCATGACCG AGGCTTACGG
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGA CGAGAGCTGT
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG
 751 GTGGGGGTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA
 801 GGGTGC GGTTTGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
 851 TGGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTCG CTGTTGGGT
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep
 1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPP RIKGKGKGV
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMP ESAGMYCLML LVFLIGVQLK
 151 SSGVSLRQVL VNRRGIRLSV WEMLSSLSGG LLFAASTDGV SWTKGLAMAS
 201 GFGWYLSLGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVFSALG
 301 *

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

m700.pep	10	20	30	40	50	60
	MDSLMTLLSVLIPMFAGFFIRV	PKPYLPALDKVLSVLVYAV	LLIGVSLRVEDLGSRLD			
g700	10	20	30	40	50	60
	MSSLMTLFSVLVPMFAGFFIRV	PKPYLPASDKVLSVLVYAV	LLIGVSLRVEDLGSRLG			
m700.pep	70	80	90	100	110	120
	DMALTVLWLFVCTVGANLLA	LAVLGKLFPPRIKGKGKGV	SVGVSGSVGQLGCVLLGFAFG			
g700	70	80	90	100	110	120
	DMALTVLWLFVCTVGANLLA	LAVLGKLSPPWRIGGKGKGV	SVGVSGSVRQLGCVLLGFVSG			
m700.pep	130	140	150	160	170	180
	KLMRDIWMPSESAGMYCLML	LVFLIGVQLKSSGVSLRQVL	VNRRGIRLSVWFMLSSLSGG			
g700	130	140	150	160	170	180
	KLMCDIWMPSENAGMYCLML	LVFLIGVQLKSSGVSLRQVL	LNRRGIRLSVWFLSSLSGG			
m700.pep	190	200	210	220	230	240
	LLFAASTDGVSWTKGLAMAS	GFGWYLSLGLVMTEAYGAVW	GSIMLLNDLARELFALAFIP			
g700	190	200	210	220	230	240
	LLFAASADGVSWTKGLAMAS	GFGWYLSLGLVMTEAYGAVW	GSIMLLNDLARELFALAFIP			

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDA	AVGVGGAT	SMDFL	LPVIQ	GAGGLE	VVPVAVS
g700	LLMKRFPDA	AVGVGGAT	SMDFL	LPVIQ	GAGGLE	VVPVAVS
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGCGCT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AACTGATGCG GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGGTGC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTTCG
801 GGGTGCGGGC GGCTTGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCG CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPPW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMPS ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSLGL VMTEAYGAVW GSIALNLDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF LTPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSA
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSV	LIPMFAGFFI	RVPKPYLPAL	DKVLSVLVYA	VLLIGVSL	RVEDLGSRLD
a700	MDSLMTLLSV	LIPMFAGFFI	RVPKPYLPAL	DKVLSVLVYA	VLLIGVSL	RVEDLGSRLD
	10	20	30	40	50	60
m700.pep	DMALTVLWLF	VCTVGANLLA	LAVLGKLFPPW	RIKGKGKGV	SVGVSGSVGQL	GCVLLGFAG
a700	DMALTVLWLF	VCTVGANLLA	LAVLGKLFPPW	RIKGKGKGV	SVGVSGSVGQL	GCVLLGFAG
	70	80	90	100	110	120
m700.pep	KLMRDIWMPS	ESAGMYCLML	LVLXIGVQLK	SSGVSLRQVL	VNRGIRLSV	WFMLSSLSGG
a700	KLMRDIWMPS	ENAGMYCLML	LVLXIGVQLK	SSGVSLRQVL	VNRGIRLSV	WFMLSSLSGG
	130	140	150	160	170	180

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	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMT	EAYGAVWGSIMLLNDLARELFALAFIP				
a700	LLFAASADGVSWVKGLAMASGFGWYLSGLVMT	EAYGAVWGSIALLLNDLARELFALAFIP				
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDF	TLPIQGAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG				
a700	LLMKRFPDAAVGVGGATSMDF	TLPIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG				
	250	260	270	280	290	300

m700.pep	X
a700	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCCTTGGC ACATATTCCA AGTTCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAAACCTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCAACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GTAAAGCGTC GCTCAACAGC AGGGCGATT TCTCGTTGAC
351 GTTGTCGTGC GGCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51  FKRFSISQHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGATT TCTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPHAGLM VVWAPNSFAS
51  FKRFSISQHT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC GGTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPHAGLMVVWAPNSFAS	FKRFSISQHT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVVWAPNSFAG	FKRFSISQHT			

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	10	20	30	40	50	60
m701.pep	70	80	90	100	110	120
	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : :					
g701	70	80	90	100	110	120
	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	: : : : : :					
m701.pep	129					
	SGTRLLSAX					
	:					
g701	129					
	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGCG ACATATTCCA AGTTGCAGGG ATACCGACGG CTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCAACTC TTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	: : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSISQT					
	10	20	30	40	50	60
m701.pep	70	80	90	100	110	120
	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120
m701.pep	129					
	SGTRLLSAX					
a701	129					
	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGtT ccaAAGCCAG TTGGA CTTCG CCCGGAGtg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTT
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CTTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAACTG CGCCGGCGGT
351 CAGGATTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:
g702.pep

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```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51  CSGLVTVPPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRADKST
101 AVLKSSIAIT GTTAPAVRIS RGV3*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALAR DSCSPGLMAKTAPASSTALSCSGLVTVPPAP					
g702	MPCSKASWTS PGVATPGIRGMPLLRLPALARDSCCKPGLMAKTAPASSTALSCSGLVTVPPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRRVISRVGMPPSTRAWDKSM AVLKSSIAIT GTTAPAVKIS					
g702	MMALGISLAI RRMASPTGV RKVISRVGMPPSTRADKST AVLKSSIAIT GTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVL RVEWGILLRW DRLX					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVPPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFPAP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFPAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDRLX
          ||||||||||||||||||
a702      RGVSLDISVLRVEWGILLRWDRLX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCAGAACGG ATTGACCGTG CCGTctgTGc gcTGTtgggT aaggCAAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIART QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGVVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYVNDNSREV
251 KVPSFDEMKG QIAGNLQAEI IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYVNDREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTTVVAQEVKRLKLDRSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYVNDREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCTT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAAACGCC TGAACCTCGAC CGGTCGGCAG
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCTT CAAAACGTT TGGCAGGCGG TAAATATGG
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
 551 TCTTGAACA ATATTCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDREVS
 251 KVPSFDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVA AAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVA AAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60

m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTVVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120

m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180

m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240

m703.pep	250	260	270	280	289
	VYYVNDREVS KVPSFDEMKGQIAGNLQAEI IDRAVGALLG KANIKPAKX				
a703	VYYVNDREVS KVPSFDEMKGQIAGNLQAEI IDRAVGALLG KANIKPAKX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq
 1 ATGAAAAA CCTGTTTCCA CTGCGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CCGGCTTGGG CAGTTATTAC
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
 251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
 301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
 401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAA TCGAAGCCGC
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCTCGCC GTTGCCGGGC
 551 TGGGATGAT GCAGACGATG ATGTTGCGCG TGCCGACCTA CCTTACGGC
 601 GCGACATCG AACCCGATT CTGCAAAATC CTCCATTGGG GCGGCTTTT
 651 AATGGTGTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTACAGCC TTGCGACAAA

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801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCGCCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGCG
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTGCG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCCTCG CCCAAACCCAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCGG TCCGCGGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCGCGG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACAGCAGCGT
1701 CCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGG ATTGGGCGG
1801 GCATCCTATG TCGCGGAAAT TTCAGGTAAG GAACCGCAA CAGAAGGCGG
1851 CGGCAGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAAGT
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCGG CCGCAGCGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCGGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATGCCGT ACCGCTTCCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1  MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLGSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLE QQLRDTGIV RIDLNYSTR CRVWDDGKI RLSDILKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLFI LHGGFLMVL PVVFCVFF YQALRLDKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALQYAS SFIFGELLLA VPFVIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSGSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRONLIWAG AYNIIAVFLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          |||
a704       MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDVFETHGGTREAVLMLGGITCAACVWLEQQLRDTGIV
          |||
a704       ELPPQEILDQIRLYDLPEVQSDVFETHGGTREAVLMLGGITCAACVWLEQQLRDTGIV

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	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKERKQYIVRLA			
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PVVFYCAVPFYQGALRDLKN			
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSL	ATNAGQGMFYFESIAML	LFLLGGRFMEHIARRKAGD			
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLIPAFCHHMPDYPDTQ	ETCEAAVVKLKAGD	IVLVKPGETIPVDGTVLEGSSAV			
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAG	TINTQSPLIIRTDR	TGGGTRLSHIVRL	LDRALAQKPR		
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAEAEQYASSFIFGELLAVPVFI	GWTLYADAHTALWITV	ALLVITCPCALSLATPTAL			
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETL	AQTTDIIFDKTGTL	TQKPAVRRISLLRGTDEAFVLA			
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRIS	DGSPDIAIKQRLNRIGEGVGA	QLTVNGETQVWALGR			
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVY	LGSQSGFQAVFYLT	DPLKDSAAEAVRQLAGKNLT	LHIL		
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGV	AHYRAQAMPEDKLEYVKALQ	KEGKKVLMIGDGINDAPVLAQAD			
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLL	NEDLRTVAHLLDQARRTHI	IRQNLIWAGAYNIIAVPLA			
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSS	LAVLGNALRLHKRGKMQSEKMPSEQX				
	790	800	810	820		

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705      95.0% identity in 238 aa overlap
                10      20      30      40      50      60
m705.pep      VENNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
                |||||
g705          VENNFLASLPFMTETRADMLISAFNPMVKAGFTVSLPLAIAASFVIGMIIAVAVALVRIMP
                10      20      30      40      50      60
                70      80      90      100     110     120
m705.pep      AGGIVRKILLKLVVEFYISVIRGTPLLVLQLVIFYGLPSVGIYIDPIPAAIIGFSLNVGAY
                :|| :| |||||

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```

g705      SGGIFQKCLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCGCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGCGGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGT
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKQWEAG FSGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705          10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||

a705.pep      70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||
m705          70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||

a705.pep      130     140     150     160     170     180
ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||
m705          130     140     150     160     170     180
ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||

a705.pep      190     200     210     220     230     239
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||
m705          190     200     210     220     230
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLIQARLEKRFDRYVAKX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCgGc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCcgcgatt tActccaacg cgggtgGAacg taTgctcggt acggtcatcg
251 ggctgGGCGC GGGTTTGGGc gTTTTATGGC TGAACCAGCA TTAtttccac
301 ggcaacCTcc tcttctacct gaccatcgGc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcgGc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCATCG CCATTGCCGC-
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRKRLS GRWLSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLI G AAIATAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEE NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGc GTTTTATGGC TGAACCAGCA TTATTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCGCGGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQNRRLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLI G AAIATAAKL LPLKSTLMWR FMLADNLAD SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING

```

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

m706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLNSEYERYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	10	20	30	40	50	60
	MNSSQRKRLSGRWLNSEYERYRRLIHAVRLGGTVLFATALARLLHLQHGEWIGMTVFVV					
m706.pep	70	80	90	100	110	120
	LGMLFQFGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVTGTASALAGWAA					
g706	70	80	90	100	110	120
	LGMLFQFGAIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTASALAGWAA					
m706.pep	130	140	150	160	170	180
	VGKNGYVPMLAGLTMCMGLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	130	140	150	160	170	180
	VGKNGYVPMLAGLTMCMGLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706.pep	190	200	210	220	230	240
	FMLADNLADCSKMI AEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP					
g706	190	200	210	220	230	240
	FMLADNLADCSKMI AEISNGRRMTRERLEQNMVQMRQINARMVKSRSHLAATSGESRISP					
m706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLGSEIRLLDRHFTLLQTDLQQTVALING					
g706	250	260	270	280	290	300
	SMMEAMQHAHRKIVNTTELLTTAAKLQSPKLGSEIRLLDRHFTLLQTDLQQTAAALING					
m706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
g706	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
m706.pep	370					
	RQHLRQSLLE TREHGX					
g706	370					
	RQHLRQSLLE TREHGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTATATGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACCTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTGCGCCT	TATCAACGGC

1137

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
 1051 ACCCGCCGCA AATGGCTGGA TGCCACAGAA CGCCAACACC TGCGCCAAAG
 1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

a706.pep
 1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYKKAVERMLG TVIGLGAGLG VLWLNQHYFH
 101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG
 151 LMRAMNVLIG AATAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
 201 RRMTREERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
 251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
 301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRWLDAHE RQHLRQSLE TREHS*

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	LGMLQFQGA IYKKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCLIGDNGSEWFD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
m706	VGKNGYVPM LAGLTMCLIGDNGSEWLD SGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRSILAATSGESRISP					
m706	FMLADNLTDCSKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRSILAATSGESRISP					
	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRWLDAHE					
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQTRRWLDAHE					
	310	320	330	340	350	360
a706.pep	370					
	RQHLRQSLE TREHSX					
m706	RQHLRQSLE TREHGX					
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1 ATGGAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTTT
201 TCTTCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTGCCG AGTGTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTTGT TTTATGTTTC ATATGGACGC
751 GGTTTTGGCG ACAAACCGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTT TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AACGCGCGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTATTTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCAG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACCCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1 MEIINDAELI RSMQRQQHID AELLTDANVR FEQPLEKNNY VLSEDETPTCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTQSA IIQPQNMDSG ILKLRVSAGE IGDIREYEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEGKSDLQ
201 IKWQGNKPIR FSIIGDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG RQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KTLVLAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGGAAATCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTTCATATG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```



```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTG AAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTTCATCCG ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCCG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSRs
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERML
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGSGT IPXSRMKII TAGLDAAPX
351 MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
m707                                EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                50      60      70      80      90     100

a707.pep                                40      50      60      70      80      90
                                GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
m707                                GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
                                110     120     130     140     150     160

a707.pep                                100     110     120     130     140     150
                                LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
m707                                LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                170     180     190     200     210     220

a707.pep                                160     170     180     190     200     210
                                GKYQGNVALSXDNPLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRsYSVHYSVXVKK
m707                                GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRsYSVHYSVPVKK
                                230     240     250     260     270     280

a707.pep                                220     230     240     250     260     270
                                WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
m707                                WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTsvgmklwtrqty
                                290     300     310     320     330     340

a707.pep                                280     290     300     310     320     330
                                KYIDDAEIEVQRRSAGWEAELRHAYLXRWQLDGKLSYKRGTMGRQSMMPAPEENGSGTII
m707                                KYIDDAEIEVQRRSAGWEAELRHAYLNRWQLDGKLSYKRGTMGRQSMMPAPEENGSGDIL
                                350     360     370     380     390     400

```

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG
          | : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAWNKTPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m707      EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          | | | | | | | | | | | | | | | | | | | | | |
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTGCTCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLVNDRAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRILNR PAESMAYFDK ALADPTYPPT YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLAA QPQFPAPFKE LARTEMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQRAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTGCTCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

```

m708.pep

```

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLKVNDAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||
g708           MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLKVNDAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              |||
g708           DALKSNPKNELAWLVRAEIYQYLKVNDAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPFPPAFKE
              |||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPFPPAFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
              |||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGTC TGCTAGGCTG
651 GAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GCGGAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLKVNDAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYFPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDEPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRLNR					
m708	DALKSDEPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPDSAEINNXYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCATTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGGCT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCCGACT TATTTTATT TTTCGCGCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggg cgcgattgTT tccggTGTGT TTTTCGCGCA
501 TAAAATGTCC CCGCTTTCGG ACACCACGGG CATTTCGCGC TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCACT GTTGGTCGTT
751 TTGSCATTGA TCGCGCTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGGCGCGGTT GCCGTAACGT ATCTGCACAG CAGCGCCGAT CTGCGTCAGC
851 TCGCGCGGTG GTTTTATGGC GGTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GCATTGCCA AACTGATTC GCGCGGCGGC TTGGAGAGTA TGTCTTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCCG TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCGTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCCGGGACT
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTGCCGT GGAGCGGTGTG
1251 CCGCGTATTT ATCAGCCACG CCCTTGCGGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCTT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MNSGAIPTLM
101 YYGFGILSPT YFYFSAFALC SVIGVSISS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEL IKNNMYTTIP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV VAMLETVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRG LLSMFFTQTI VILGMSLGL LFALGVIPSL LEAVRTFLT N

```

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVFVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTCATTGG
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTATT TTTCCTCCTT
 351 CGCGCTGTGT TCCGTATCG CCGTGTCCAT CGGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGCGC GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CGCGATTGTT TCGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGCGC TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCAGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
 701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGCCTT GTTGGTCATT
 751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTGCGCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAA
 901 GATGTTGTCA AACTGATTTC GCGCGCGCGT TTGAAAGTA TGTTTTTCAC
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGC
 1001 TCGGTGTGAT TCCTTCCTG TTGGAGGCCA TCCGTACCTT CTGACGAAT
 1051 GCGCGACGCG CGACGTTTCA CGTTGCCATG ACTTCGCTCG GGGTTAATTT
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA
 1151 AACCCTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
 1201 CTGGAAGATG CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
 1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATCGGT
 1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQFA
 151 DMAMTAGAIV SGAFVGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTIP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGF LESMFFTQTI VILGMSLGL LFALGVIPSL LEAIRFTLN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVFVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	70	80	90	100	110	120
	DMQGMIGALNQGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQGMIGALNQGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	130	140	150	160	170	180
	SVIGVSIGSSLTTCATVGVA FMGMAAFQADAMTAGAIVSGAFVGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTTCATVGVA FMGMAAFQADAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	190	200	210	220	230	240
	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLF	TMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
g709	SLIPFALLVILALMRVNAVAMLF	TVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK				
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAIRTFLTNAGRATFSVAM				
g709	DIAKLISRGGLESMTFTQ	TIVILGMSLGGLLFALGVIPSLLEAVRTFLTNAGRATFSVAM				
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPLVPWSVCGVF				
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLS	SRTLEDAGTVINPLVPWSVCGVF				
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLT	SKKX				
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLT	SKKX				
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATGCGG CCATCGTNGT GCTGATTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGN CNNGATTGTN NNGNCGCAT TNTNNGCGN
501 CAAATGTCTN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTGC
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCCT GTTGGTCGTT
751 TTGGCATTGA TCGCGCTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCCA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGCGGCT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCCTT GGATGAGCCT TGGCGGGCTG CTGTTTGAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCNGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGCG TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSISS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXIV XXAXXGXKMS PLSDTXGKSA SIVGIDLFH IKNNMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV AVAMLFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQTI VILGMSLGG L FALGAIPSL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTII	SLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIY	LEFFIGLM	VSALMM	SGAIP	TLMYYG	FGLISPTYFYFSAFALC
m709	DMQQGMIGALNQGMGAIY	LEFFIGLM	VSALMM	SGAIP	TLMYYG	FGLISPTYFYFSSFALC
	130	140	150	160	170	180
a709.pep	SVIGVSI	GSSLTTCATV	GVAXMGXXXAF	XAMXXXXXIV	XXAXXG	KXKMSPLSDTXGXSA
m709	SVIGVSI	GSSLTTCATV	GVAFMGMAAFQ	ADMAMTAGAIV	SGAFFG	KXKMSPLSDTTGISA
	190	200	210	220	230	240
a709.pep	SIVGIDL	FEHIKNM	MYTTPAW	LISXXLM	LXLLPS	VAAQDLNSVESFRSLEATGLVHCY
m709	SIVGIDL	FEHIKNM	MYTTPAW	LISAALM	LWLLPN	VAAQDLNSVESFRSLEATGLVHGY
	250	260	270	280	290	300
a709.pep	SLIPFALL	VVLALMR	NAVAV	MLFTVIA	AAVAVTYL	LHSTPDLRQLGAWFYGGYKLEGEAXX
m709	SLIPFALL	VILALMR	INAVV	AMLFVM	VAVAVTYL	LHSTPDLRQLGAWFYGGYKLEGEAFK
	310	320	330	340	350	360
a709.pep	DIAKLIS	RGGLES	MFFTQ	TIVILG	MSLGGL	LFALGAIPSLDDAVRSFLT
m709	DVVKLIS	RGGLES	MFFTQ	TIVILG	MSLGGL	LFALGVIPSLLEAIRFTLT
	370	380	390	400	410	420
a709.pep	TSVGVN	FLIGE	QYLSIL	LSGET	FKPVYD	KLGLHSRNL
m709	TSVGVN	FLIGE	QYLSIL	LSGET	FKPVYD	KLGLHSRNL
	430	440	450	460		
a709.pep	IXHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GWGTGLTLSKKX
m709	ISHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GWGTGLTLSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCGGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCAGCTTT	GGAGCAGTTG
151	GCTCAGATTT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAAAT	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGCC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

1146

301 TTGAAACACT GCAAAGAAAT GTTGAACAA AAAGACAAAG AAATCGAGCT
 351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 2386; ORF 710>:

m710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
 101 LKHCKEMLEQ KDKEIELLRK LTETV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2387>:

a710.seq
 1 ATGGAAACCC ACGAAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG AGGCGAAACG CAGTTGAATA TCCCGCGTTT GGAGCAGTTG
 151 GCGCAGATTT TCAAAATTGA TATGTGGGAC TTGCTCAAAT CGGGCGGCGG
 201 CGGGATGGTG TTGCAGATTA ACGATGTGGA TACCAACAGC GGGGAATTTG
 251 CAATCTATAC CGCTCAGGAT GCATCNGGTA AAGCTGGATT TGTTAAAATG
 301 GAATTTAAAC ACTGTAAAGA AATGTTGGAA CACAAAGACA AAGAAATCGA
 351 GCTGCTCCGC AAGCTGACCG AAACCGTTTA A

This corresponds to the amino acid sequence <SEQ ID 2388; ORF 710.a>:

a710.pep
 1 METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51 AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
 101 ELKHCKEMLE HKDKEIELLR KLTETV*

a710/m710 85.7% identity in 126 aa overlap

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR					
m710	LLKSGGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMELEHKDKEIELLR					
	70	80	90	100	110	
a710.pep	KLTETVX					
m710	KLTETVX					
	120					

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAACTTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGCTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCCTATAAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSQGS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRRTPAHSAL DGLVYRYDDP FWATFYPPNG YNCRCVIAL SERDVERQQR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFdynAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAACTTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```

901 CCGGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

a711.pep

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPASAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRDLIDGK
301 PDKEQIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDLTVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFSTSFKQLEKEFYEVKQRDLIDGK					
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFSTSFKQLEKEFYEVKQRDLIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDLTVKQVDSREGQNFDD					
m711	PDKEQIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDLTVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
1  ATGATGCCCC ATATTGATT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAATGCGGA CATTGCCACG GCCTTGTTCCA AAGTGGCGGG
651 CAAGCATTAT CACATTATT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGGC GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GGCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGTCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTGA
1401 TTTGATTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
1  MMFHIDFTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLKIKGLAV TPDAQWPLFA ECNNALYNGT TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPDRKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNLGLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```
m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGCGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCGG ACGCTTACCC CAAAAGGGC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```
m713.pep
1  MQNNSYGYAV SVRVGKKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSESCV VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGLTVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFIA QSHGRSGDSA KHDLEWVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMSLRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKKQAETAVF E*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```
a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGCGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCGG ACGCTTACCC CAAAAGGGC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKVVKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FLSRMDGTQ TELRLKEDI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGK GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSGESCE					
m713	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSGESCE					
a713.pep	70	80	90	100	110	120
	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	70	80	90	100	110	120
	VVIDGQIVMTGIIGSQRHGKSKGSRRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
a713.pep	130	140	150	160	170	180
	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGVD					
m713	130	140	150	160	170	180
	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGAD					
a713.pep	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
m713	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
a713.pep	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
a713.pep	310	320	330	340	350	360
	VHVIDDEHGIDAVFFLMGRRFMSRMDGTQTELRLKEDIWTPDAYPKKAEAAARKRKGR					
m713	310	320	330	340	350	360
	VHVIDDEHGIDAVFFLMGRRFMSRMDGTQTELRLKEDIWTPDAYPKKAEAAARKRKGR					
a713.pep	370	380				
	KGVS HKGKGGKKQAETAVFEX					
m713	370	380				
	KGVS HKGKGGKKQAETAVFEX					

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERLVGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCAGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERLVGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW					
	10	20	30	40	50	60
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
a714.pep	AGDRLAPQEIIMVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					
	130	140	150	160	170	180
a714.pep	AGDRLAPQEIIMVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNRVGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGGLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAA ATATTGCTGC CGCACTCGCC GGTGCTTAT CCCTGTCTCT
 51 GGCCGCCGCG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

-- This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAAHKPASNATGVQKSAQGSAGGSCGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60

	60	70	80	90	100	
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
 51 GGCCGCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
 201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
 301 TCTAAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
 101 SK*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60

	70	80	90	100
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX			
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCCGCGG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTCAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CCGCCGTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CGCGCGCCGT  TTTGCCCGCC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGGCATT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGCTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAGAACTAC  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCGC
1001  cgtggtttta  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCGTCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGCGCGCG
1151  CGGTTGCTTG  TGCCGCCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTT  TGCTTGGCCT  CCTCGCGCGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCCTGTTT  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYAAAD  KDTLFKTLFL  PFLLFSAAIA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSFLPIRFL  LVLRMERAL  AFSSAQLVPK
151  LAIILLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAFFSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKKY  AGLEQLGVYS
251  MGISFGGAAL  LQSIFFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIFSP  LASLLLPENY  AAVRFTVVC  MLPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCCGCGG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTCAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGCTGCGCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATTC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCCTGA  CCGCCGTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CACGACCCGT  TTTGCCCGCC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCCGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGGCATT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAGAACTAC  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTC  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCGTCTGCTG  CTGGGGCTTG  CCGTGCCTGC  CGGCGGCGCG  CGCGCGCGCG
1151  CGGTGCTGCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCCCGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTGACAC  AAAGTGTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PELLSSAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVVK
151 LAILLPLLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAARDKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAILLPLTVGLLHFPANTSVLTAVALA					
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTG CCGCCGCTGC

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1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACCTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTA CCGCTGGCA AACCTTGCCG
551 CCGCCGCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCGTCCGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTCTCT GAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCGCCCT GCTTGCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCGCTCC GGTTCATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGCGCGG CGCGGCGCGG
1151 CGGTTGCTCG TGCCGCTCA TTTTGGCTGT TTTTGTTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATGTGTC TGCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAACTA CCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAATGTTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV IMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLEKTLFL PLLSAAAI AALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSELPPIRFL LVRMEGRAL AFSSAQLVSK
151 LAILLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPSSAVLH RGLRYGPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFSIFSTVW TPYIFRAIEA NAPPARLSAT AESAALLAS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVEKTE
401 SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

          10      20      30      40      50      60
a717.pep  MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
          |||
m717      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
          10      20      30      40      50      60

          70      80      90      100     110     120
a717.pep  YVREYYAAADKDTLEKTLFLPPLLSAAAI AALLSRPSLPSEILFSLDDAAAGIGLVLE
          |||
m717      YVREYYATADKDTLEKTLFLPPLLSAAAI AALLSRPSLPSEILFSLDDAAAGIGLVLE
          70      80      90      100     110     120

          130     140     150     160     170     180
a717.pep  LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
          |||
m717      LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
          130     140     150     160     170     180

          190     200     210     220     230     240
a717.pep  NLAAAFLLFQNRCLKAVRRAPSSAVLHRLRYGPIALSSIAWGLASADRLFLKKY
          |||
m717      NLAAAFLLFQNRCLKAVRHAPSPAVLHRLRYGPIALSSIAWGLASADRLFLKKY
          190     200     210     220     230     240

          250     260     270     280     290     300
a717.pep  AGLEQLGVYSMGISFGGAALLFSIFSTVWTPYIFRAIEANAPPARLSATAESAALLAS

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1159

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLVVRKTRPIALAT
|||||
m717      ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAAANLLLLGLAVPSGGARGAAVACAASFVWFFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717      LGALAAANLLLLGLAVPSGGARGAAVACAASFVWFFVFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLFHYLKKQGFPPLX
||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAVYLAGCILRHRKDLHKLFHYLKKQGFPPLX
           430      440      450      460      470

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g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAATGG  GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA  CGCTTCTCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TCGGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCAGAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCAATCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVRNF IHRQSWFKW DKDNGLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQRNG LFRTLSWLYM FKHYAVHDFE EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GOTLTSGADG KSSTNALGNI HNEVRDLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVGVQ
251 IPESWVRDKL VIPDVQEGEA VLVQRVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVROA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILQGDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGGCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGGCG AAACCATCAC AAGCCAAATC
1051 ATCCGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHLEFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLMD DAVGHGFSAL EVEWVFS DGL
151 YLPNFIHRP QSWFKWDKDN GLLLRTRNPE EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMA DWCEKS
301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFPLQINYP HADPNRVPKF EFDTRPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFS	SALEVEWVFS	SDGLYLPRNFIHRPQSWFKWDKDN	GLLLRT		
m718				SDGLYVPRNFIHRPQSWFKWDKDN	GLLLRT	
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRV	QQARNGLFRTLSWLYMFKHYAVHDFAEFLE	LYGMPI			
m718	RENPEGEALWPLGWVVHTQKRSRV	QQARNGLFRTLSWLYMFKHYAVHDFAEFLE	LYGMPI			
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPF	LQMA DW				
m718	RICKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMA DW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGFFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGFFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVVDVGQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVVDVGQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDNFVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDNFVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
m718	340	350	360	370	380	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATCGGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAT ATGGGGACGC
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCA ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCGCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAA C GGGCTGCTGC TGCCTACCG CGAAATCCG GAAGCGGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCGCTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCGTC TTCGAGCGGT GCGGGAATC GGTCAACAG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAG TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGCGCGCGG TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAA CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC CGGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKN KTKIQPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDSDIAAN MGRKRALLT LNRVRAPPRN
101 ATPEEEEKLS QAYEMMSDLP TLEDLIMDLN DAVGHGFSAL EVEWVSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGTTATSNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

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351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVI PD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGCGCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGGCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCT TTCGAGCGGT GCGGGAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGCGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGCGCG AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGTACGGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep
1 MEPIMAKKNN RTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFADI EERDSIAAN MGRKRALLT LNWRVAPPRN
101 ATPEEKLSL QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EWEVVFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN PEGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVI PD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

a718/m718-1 99.0% identity in 526 aa overlap

a718.pep	10	20	30	40	50	60
m718-1	10	20	30	40	50	60
a718.pep	70	80	90	100	110	120
m718-1	70	80	90	100	110	120
a718.pep	130	140	150	160	170	180
m718-1	130	140	150	160	170	180

1163

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMDWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTATSNPFLQMDWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
m718-1	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGGC	GCAGCGGCAA	GGCATCACAA	AATGATTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCGGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCTG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGCGATT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTTCAG	GCAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

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1301 TAACGTTGGA TAACGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTCGGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGACAG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCAATGG GAAAACTGCG CGGTAGCGGG CTGATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAG GGTTCGCGT GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTGTAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCCTAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGCGGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAAGTG
2051 CGATGGCGTC GGCAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CCGCGTGGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
1  MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL EROSHTYALT
51  GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIAATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSGLDGL TFEVRDMVRE LPSLLSAAQO AGMNGVGGLD YLLSLLQSAA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLNDGK IAKNNEARML
451 SAAQQEQEQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WKGASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLESTQTA
651 AYQAAIQQOT AAYQAAALQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
1  ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51  CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGACAG TGCAAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGCACCC TGTTCGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTCCTT GAAAACGCCT
401 TTTTGGTCTG GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTGTTGA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCGGTTT TTTGATTGAG ACAAATTGC CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTCCGCCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCTG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

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851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCCTCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGCGCG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 CGGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

-- This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIFVF ENAFLEVEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPQRFR
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAQVQF VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGATATC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGCGGCTC ATCAACCAAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTACGCG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACCTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNRNLRLT AKQVQFVAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAASGGL TANAVYTEAY QTAESLRAAA
101 GRNLALVA AV INQKPPPLIVR QAPIDGTI HQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

          250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRNLRLTAQVQFVAQAVRLLSTSSLL
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a720      GLQNRNLRLTAQVQFVAQAVRLLSTSSLL
          10      20      30

          310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a720      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          40      50      60      70      80      90

          370      380      390      400      410      420
m720.pep  QTAESLRAAAGRLNALVAAVINQKPPPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a720      QTAESLRAAAGRLNALVAAVINQKPPPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
          100     110     120     130     140     150

          430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

```

1166

|||||
a720 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAACGCCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGCAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGCT GGGCATGTCC GCGGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYWLTTEE
51 NGHDAVALLAN SSRNQLVVYD EHQTLYKEKN GQAPAPAGWM RWLEFTPCKGM
101 FAEVEWTDKA AAALAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPEEQN FMKELLQOLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTCGCG
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
151 AACGGTCATG ATGTGCGGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCGCGCCT CGTGGAAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCA
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAACGCCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGTAA
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAATGCT GGGCATGTCC GCGGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRVAVDGRPT DVPAWYLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRVAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRVAVDGRPTDVPAWYLTEENGHDVALLAN					
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNQPPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	70	80	90	100	110	120
	SSRNQLVVDYEHQTLYKEKNQPPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	190	200	210	220	230	240
	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGVLKQPGGLAFLTGFI					
m721	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAGVLKQPGGLAFLTGFI					
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGGKX					
m721	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGGKX					

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCGC ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GCGCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAA GCGGCGCGCA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCAT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGCGCCAAT GTGCGGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGCGCGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAA GCGGCGCGCA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRPPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDL LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCGGAACACC TTATTTTAC  CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTC GCCATAGCAC GCAGCAGGTC GAGCAGCTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTAATCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTTCAGCAT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGCGGCG GGTTCGCGCG GTTTCGTGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLLSSA SSADS AFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
a  TACTCAAACCTCATTTAACCGCTTTTTTTGCCGTGTTTGACGATTTTATAGCCGCTTTGG
   M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTTCGGGGAAAAATCACGCTGGTGGTGTCTCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
a  GACGCGCGCCGGAAGCCCTTTTGTAGTGCACACACAGCAGGCTCGGCTATGTCGCG
   L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCCGACGAAACCCTGCAAGACCTGAACATTGTCAGGAATAC
121  -----+-----+-----+-----+-----+-----+-----+-----+ 180
a  CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
   V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+-----+-----+-----+ 240
a  CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCGGTTA
   G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTGGAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -
      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCACTAATTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -
      ATCATTGAGGCCGATTGCGACGTGTACCGGGTAACTGCAAAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+ 420
      TAGTAACCTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -
      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAAGTGTGACGGCGCAA
421 -----+-----+-----+-----+-----+ 480
      CGGTGCCTACGTTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACGCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -
      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGGTACCGGCAGCTCCCGCGCTGCCCTCGGTGGAAATCG
a      G Q I N G N G G M A V E G G D G A T F S -
      GCGCATGTTAACCAACGGGCGGCAGCTTTAACACCGACGGCGACGTTGGTGGCCGCAAT
541 -----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCGTCGAAATTGTGGCTGCCGCTGCACCACGGCGCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -
      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601 -----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCTAGCCGCGTTTTGGAATGGCCGCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -
      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

```

m724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKENAPL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

```

a724.seq
1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGACCGG GTTAACGTGA
401 AACAAATACG GGTAAATGCG GCCACGGATG CCAAATTTAA CGTCCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```


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501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
 551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
 601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAACCTT
 651 ACCGGCGGAA CCGGCATAG

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

a724.pep

1 MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
 51 LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKLNK
 101 PGETAIFNHE GAKIVIKQ GK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
 151 VETSAVLTAQ GOINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
 201 ISLRQHPHTD SIGGKTLPAE PA*

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPKGETAIFNHEGAKIVIKQ GK					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPKGETAIFNHEGAKIVIKQ GK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGOINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGOINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

m725.seq

1 ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
 51 GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
 101 TTGAGCCTGC CAGCACCGGC GCGTATGCG GACGTTATCA GGATACCGCC
 151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
 201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
 251 GCGCTGTTGC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
 301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
 351 GCAAACGCGC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
 401 ACACCTGCGG GTTGGAAGAT GACCGCTACC CCGAACGCAC CGACAATCCC
 451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
 501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
 551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

m725.pep

1 MVRTVKS YNG EADDLAGQIH TLPVWV TYG GSKVEPASTG GVCGRYQDTA
 51 EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLL DGQRLGFADS
 101 RGLVPKAVRA IANHLVQNA AVSIYAVEYA IRENTCGLEN DRYPERTDNP
 151 DDPNHIFTKY QGTLSEPPD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCAGAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTAAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAATC AGCAAAGCCG CGCCGCGCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAACAGC
301 CTCTGGCGG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCGCGC AGGGGCGTGG AATTGGACGT TTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCGC GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSEDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCGGCAT
51  CCCCAGAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTAAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCGCG CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAACAGC
301 CTCTTGGCGG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCGCGC AGGGGCGTGG AATTGGACGT TTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCGC GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
1  MTIYFKNGFY DDTLGSIEPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTTPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVVEKSARLA VAAGAIIGKR QLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*
```

a726/m726 95.5% identity in 201 aa overlap

```

      10      20      30      40      50      60
a726.pep MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726     MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEDY
          10      20      30      40      50      60
```

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```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:::|||||:||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKINTI
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKINTI
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTNIGX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          ETAPGLDALEKEIEEWTNIGX
              190      200

```

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPFD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTGTC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10          20          30          40          50          60

              70          80          90          100         110         119
a727.pep   YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRKLTENKKEIENV-LTQDRKNAGGGC
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEEAKKYEVKAHAVGMALAKKQAEVSRKLT--RDLCKIPFPDPSRNPNTGF
              70          80          90          100         110

              120         130         140
a727.pep   IDGFGHHGLQLYKRALGYGNX

m727      RLFSPPQIPPNTQIPPX
              120         130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTTGGT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TTCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

1175

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1  MEKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVIFYQN
251 MRELMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
301 IAQSSTVALK ADGVTADMT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNPNAFVAKLARLFRNA					
g728	MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGVSFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGVSFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVIFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF					
g728	DSRDYVIFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

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```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360
           370
m728.pep  YAEAAARRSGGRRDLSHX
           |||||
g728      YAEAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCAGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTT
401 CGCAACGCTC GCCGGAAGCG TTTGTAAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGCTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTGGAAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGQYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      WLDDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLLVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSLLVVGVDADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTDQMOTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSTVALKADGVTDQMOTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAAARRSGRRDLSHX					
m728	YAEAAAARRSGRRDLSHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA  CATTGAAAAC  TACCTTGACC  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCTCAATA  CGAGCAGCCC  AAAGTCGAAG
101  TTGCGGAAAC  CTTCCAAAAC  GACACATCGG  TTTCTTCCAT  CCGCGCGGTT
151  GATTTGGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201  CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACAGCC  GTATTGAACA
251  GCGAAATCTA  CCGCAAAACA  TACATGATCG  AGCGCAACAA  CCTCCTGCCC
301  ACGCTTGCCG  CCAATGCGAA  CGGCTCGCGC  CAAGGCAGCT  TGAGCGGCgg
351  caaTGTCAGC  AGCAGCTACA  ATGTCGGAAT  GGGTGcGGca  tCTTACGAAC
401  TCGATCTGTT  CgGGCGCGTG  CGCagcaaca  GcgaagcAGC  ACTGcaggGC
451  tATTTTGCCA  CGGTTGCCAA  CcgCGATGCG  GCACATTTGa  ttCtGATTGC
501  CACCGTTGCC  AAAGCCTATT  TCAAcgaGcG  TTATGCCGAA  AAAGcgatgT
551  CTTTGGCGCa  gcGTGTCTTG  AAAACGCGCG  AGGAAACCTA  CAAGTGTGCC
601  GAATTGCGGT  ACAAGGCAGG  CGTGATTTCG  GCCGTGCCCC  TGCGCCAGCA
651  GCGAGCCTTG  ATTGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCa
701  gcCGGCAACA  GGCGCGCAAT  GCCTTGGAAC  CCTTGATTAA  ccGTCCGATA
751  CCCGAaGACC  TGCCCCCGCG  TTTGCCGTTG  GACAagcAGT  TTTTGTGTA
801  AAAATGCCT  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGACA
851  TCCGCGCGC  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901  gcgCGCGCCg  ccTTTTTCCC  GTCCATCCGC  CTGACCGGAA  GCGTCGGTAC
951  GGGTTCTGTC  GAATTGGGCG  GGCTGTTCAA  AAGCGGCACG  GCGGTTTGGG
1001  CGTTCGCTCC  GTCTATTACC  CTGCCGATTT  TTAATTGGGG  AACGAACAAG
1051  GCGAACCTTG  ATGTGGCAAA  ACTGCGCCAA  CAGGCACAAA  TTGTTGCCTA
1101  TGAATCCGCC  GTCCAATCCG  CCTTTCAAGA  CGTGGCAAA  GCATTGGCGG
1151  CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAGCCGC
1201  GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGA  CTGCGTTACA  AACACGGCGT
1251  ATCCGGCGCG  CTCGATTGTC  TCGATGCGGA  ACGCATCAGC  TATTCGGCGG
1301  AAGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTCCGAT
1351  TTGTACAAGG  CGCTCgacGG  CGGATTGAAA  CGGGATACCC  AAACCGGCAA
1401  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFQN  DTSVSSIRAV
51  DLGWHDFYAD  PRLOKLIDIA  LERNLSLRTA  VLNSEIYRKQ  YMIERNLLP
101  TLAANANGSR  QGSLSGGNVS  SSYNVGLGAA  SYELDLFGRV  RSNSEALQG
151  YFASVANRDA  AHLILIATVA  KAYFNERYAE  KAMSLAQRL  KTREETYKLS

```

m729.seq

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

m729.pap

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

m729.pep MDTLKTTLTLSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g729 MNTLKTLLTSLVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
 10 20 30 40 50 60

1179

m729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
g729	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNVS					
m729.pep	130	140	150	160	170	180
	SSYKVLGAASYELDLFGRVRSSEALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	130	140	150	160	170	180
	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLIATVAKAYFNERYAE					
m729.pep	190	200	210	220	230	240
	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAARSREQARN					
g729	190	200	210	220	230	240
	KAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQOEALIESAKADYAHAARSREQARN					
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	250	260	270	280	290	300
	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	310	320	330	340	350	360
	ARAAFFPSIRLTGSGTGSVELGGLFKSGTGWAFAPSITLPIFTWGTNKANLDVAKLRQ					
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
g729	370	380	390	400	410	420
	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
m729.pep	430	440	450	460		
	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	430	440	450	460		
	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGATACTA CATTGAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51 ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCTGCG AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGAAT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTCCGCA GCACCGCCAA CCGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAGCCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GGCGCGCAAT GCCTTGCGAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTTGA
801 GAAGCTGCCG GCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCGG CCTTTTCCC ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGGTTGGT
1001 TGTTCCGACC TTCCATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG

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1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAG AAGCGTTGCG TTTGGTTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTGCGCGG
1301 AAGTGCGGCG TTTGTCGGCA CAACTGACCC GCGCCGAAAA CTTGCGCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRLV KTREETYKLS
201 ELRYKAGVIS AVALRQREAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPAFLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

```

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
m729	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD
a729.pep	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS
a729.pep	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE
a729.pep	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQREALIESAKADYAH AARSREQARN
m729	EAMSLAQRLVKTREETYKLSELRYKAGVIS AVALRQREALIESAKADYAH AARSREQARN
a729.pep	ALATLINQPI PDDLPAFLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA
m729	ALATLINQPI PDDLPAFLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ
m729	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA
m729	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA

1181

```

          430      440      450      460
a729.pep  LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m729      LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

```

g730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCTCGCA  CTCATACAGC  CCGCCCTCGC  GCGGGA CTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CCGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGCAGC  GTTTCGGACC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTG GTT  ACACCGTCCG  CTTTTCGGGA
301 CACGGACACG  AAGAACACGC  CCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCAATT  ACCCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCCGCA  GTATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATTC  GACAACTACA  ACAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCAACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGCGCAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCGC  CGCCATCGGC  GGCTTGGGCA
851 GCGCGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGCGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAAACCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACC GTTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCTGA  TTTCCAACCG
1251 CATCCACCGG  TTTTATTCGG  ACGGCAAATG  GATTAAGGCG  GAAGATTTAA
1301 AAGCGGGAAG  CCGGTGTGTA  TCCGAAAGCG  GCAAAACCCA  AACC GTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTCGCG  AAGGAAAGCA  ATATTTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGGAAATGGA  CACC AAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```

g730.pep
1  VKPLRLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  N  LLIQAAAIQ  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADANRK  MFEHNAKLDR  WGN SMEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPI  PAEGKF AAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLT KAAK  PGKAAVSGDF  SKSYTCSFHH
351 STLVKTAGDY  KAIAHIQAGD  RVLSKDEASG  ETGYKPV TAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYS DGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLT VADWH  TYFVKGNQAE  TEGVWVHND  C  PPKPKPTNHA
501 QORKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

```

m730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGCGCGCA  CTCATACAGC  CCGCCCTCGC  GCGGGA CTTG  GCGCAAGACC

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1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGACG GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGG ATGCCTACGA CGGCCGGAAG
451 GCGGCAATT ACCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCGCA
551 GCATCCGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGCGGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCGCGCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTGTA CCGGTGGATA
901 CAGGAAATC CCAATCGCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAACG TGCAGATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMG NLLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPKNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m730      VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90      100     110     120
g730.pep  VSDRTGKINVIQDYTHQMG NLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m730      VSDRTGKINVIQDYTHQMG NLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90      100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m730      KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNSEFVNGVAAGALNPFI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m730      DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI
          190     200     210     220     230     240

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730						
	250	260	270	280	290	300
	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYTCSEFHGSTLVKTADGY					
m730						
	310	320	330	340	350	360
	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKAAVSGDFADSYKKKLALSDSARQLYQN					
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVYTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNLFNLQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TGCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGCGCCGCA  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCACAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTCCGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCAATT  ACCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAAACT  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCCCG
701 CCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCACAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCTT
951 GCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACCTAG
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTT  ATCTGGAAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIK  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRG  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAPFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGP
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADENRK  MFEHNAKLDR  WGNSEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQONQNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFFDRTS  NPKYNPVK*

```

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRLRIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRLRLNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTAAKPGKAAVSGDFSAAYNTRTRTKVTETEGLN					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGHLFPKGPKGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGHLFPKGPKGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gattttcag cgttttcatg CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC
101 TCTCTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGCGCGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCTGCGGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCTCTC TTCCGACGTT GCCGCATCCG

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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

g731.pep					10	20	30
					DFRAFSCE	GLSVRVRNLDGGKIALRLDGR	
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	GLSVRVRHLD	DSGKVALRLDGR				
	20	30	40	50	60	70	
g731.pep		40	50	60	70	80	
		RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX					
m731		RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX					
		80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTV	PVLSLAACAV	PEAYDDGGRGHMPPVQNQAGTADFRAFSCE	GLSVHVRRL		
m731		MNIRFFALTV	PVLSLAACAV	PEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	GLSVRVRHL		
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLD	GRRAVLSSDV	AASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE			
m731		DSGKVALRLD	GRRAVLSSDV	AASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE			
		70	80	90	100	110	120

a731.pep TSCRARX
 |||||
 m731 TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTGGC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGCGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTGCGG AGTTGAAAAC GATTCGGATG ACGgtatTGG TcaaTTCGG
951 TTCggcttCC CGTTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCA TCGCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCGG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGCGACCTG
1201 LTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgccGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGCGC GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGTT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

```

g732.pep
1  MSKPVFKKIA  LYTLGAISGV  AVSLAVQGF  AEKDGRDNEV  LPVQSIRTMA
51  EVYGOIKANY  YHDKPDADLF  EGAMKGMVAG  LDPHSEYMDK  KGYAEIKEST
101 SGEFGGLGME  IGQEDGFVKV  VSPIEDTPAE  RAEVKSDFI  VKIDNVSTRG
151 MTVSEAVKMK  RGKPGTKITL  TLSRKNADKP  IVVNLTRAI  KVKSVRHHLI
201 EPDYGYIRVS  QFQERTVESV  NTAAKELVKE  NKGKPLKGLV  LDLRDDPGGL
251 LTGAVGVSA  FLPSEAVVVS  TKGRDGDGDM  VLKAVPEDYV  YMGGDPLAG
301 IPAELKTIPM  TVLVNSGSAS  ASEIVAGALQ  DHKRAVIVGT  QSFSGKSVQT
351 LIPLSNGSAV  KLTTALYYTP  NDRSIQAQGI  VPDVEVKDKE  RTFESREADL
401 VGHIGNPLGG  EDVNSETLAV  PLEKDADKPA  AKEKGKKKKD  EDLSSRRIPN
451 PAKDDQLRKA  LDLVKSPEQW  QKSLGLAAKK  FVSNKDKKDK  K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

```

m732.seq
1  ATGTCGAAAC  CTGTTTTTAA  GAAAATCGCA  CTTTATACTT  TGGGTGCAAT
51  CAGCGGCGTG  GCCGTCAGTC  TGGCGGTGCA  GGGTTTTGCC  GCCGAGAAGG
101 ACAGGCGGGA  TAACGAAGTC  CTGCCGGTGC  AATCCATCCG  CACAATGGCG
151 GAGGTTTACG  GTCAAATCAA  GGCAAACTAC  TATCAGGACA  AACCCGATGC
201 CGATTTGTTT  GAAGGTGCGA  TGAAGGGTAT  GGTGGCCGGT  TTGGATCCGC
251 ATTCGGAATA  TATGGATAAA  AAAGGTTATG  CCGAGATAAA  GGAGTCCACC
301 AGCGGCGAAT  TTGGCGGCTT  GGGGATGGAA  ATCGGGCAGG  AAGACGGATT
351 TGTCAAAGTG  GTTTCGCCGA  TTGAGGACAC  GCCTGCCGAA  CGGGCGGGGG
401 TGAAAAGCGG  CGATTTTCATT  GTGAAAATCG  ATAATGTTTC  GACACGCGGC
451 ATGACGGTCA  GCGAAGCGGT  GAAGAAAATG  CGGGGCAAGC  CGGGTACGAA
501 GATTACTTTG  ACGCTGTCGC  GCAAAAATGC  CGACAAGCCG  ATAGTCGTCA
551 ACCTGACCCG  TGCCATTATT  AAAGTGAAAA  GCGTCCGCCA  TCACCTGATC
601 GAACCCGATT  ACGGCTATAT  CCGCGTGTGC  CAGTTCCAAG  AGCGGACGGT
651 CGAAAGCGTC  AATACCGCCG  CAAAAGAGCT  GGTAAGGAA  AATAAAGGAA
701 AACCGCTCAA  GGGGCTGGTG  TTGGATTGTC  GCGACGACCC  CGGCGGGCTT
751 TTGACTGGCG  CGGTCGGCGT  GTCGGCGGCA  TTTCTGCCGT  CTGAAGCAGT
801 CGTCGTCAGC  ACCAAGGGAC  GCGACGGCAA  AGACCGCATG  GTACTGAAAG
851 CCATTCCTGA  AGATTATGTG  TACGGGATGG  GCGGCGATTC  GTTGGCGGGC
901 ATTCTGCGG  AGTTGAAAAC  CATACCGATG  ACGGTATTGG  TCAATTCCGG
951 TTCGGCTTCC  CGGTCGGAGA  TTGTCGCAGG  TGCATTGCAG  GATCATAAAC
1001 GCGCGGTCA TCGCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1187

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CTGCCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

```

m732.pep
1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEFGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSGKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSFEQW QKSLGLAAK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEFGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEFGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
	190	200	210	220	230	240
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
m732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSGKGSVQTLIPLSNGSAV					
g732	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKKKX					
g732	PVSNDKKDKKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTGTGTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 GAACCAAGCG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTTCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGGTGTGCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAGGAA AATAAGGAA
701 AACCCTCAA GGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTGCGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CCGTCTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCTGCCG AGTTGAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCTCGGAGA TTGTCGCAGG TGCAATGCAG GATCATAAAC
1001 CCGGGTTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGGATTGTT
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAGC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGATTATAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGIVRSV QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAUGVSAA FLPSEAVVVS TKGRDGDKDM VLKAVPEDYV YGMGGDSLAG
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFQKGSVQT
351 LIPLNSGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDKD KDKK*

```

1189

a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPVQSIRTMAEVYGGQIKANY					
	10	20	30	40	50	60
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAV					
	250	260	270	280	290	300
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHRKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHRKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHRKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHRKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
a732.pep	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
m732	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
m732	KLTTALYYTPNDRSIQAQGIQVDPVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	370	380	390	400	410	420
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
a732.pep	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					
a732.pep	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51  GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTATACC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCATTG GGAAGTCTGC

```

1190

251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep
 1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq
 1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC
 251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep
 1 MMNPKTLSRL SLCAAVLALT ACGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

m733.pep	10	20	30	40	50	60
	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
g733	10	20	30	40	50	60
	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733.pep	70	80	90	100	110	120
	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
g733	70	80	90	100	110	120
	YFAEAANKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEEKRLFPESGVFMDFLMKTGKG					
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq
 1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC
 251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

```

1  MNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGKNDTDS
51  LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGKNDTSLGKQTEKMEK
              |||||
m733           MNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGKNDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              |||||
m733           YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              |||
m733           GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTGG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTGCTT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHQV ALNQCIKKYG AQGQCGLETV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCT
51  GAACAATACC TGTGTGCGCG TGGCATACCC GAAAGCCTTG GCGCGCTGC
101 GTGTGACAA CGCCGTCTGT ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGAA ACAGTGATAT GCACATCTTC TTCTTATTAC GCGGGAATG
251 TCGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAVV ITS PRFTSVH
51  QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
              :|||
g734           VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```

1192

	40	50	60	70	80	90
m734.pep	GALRVDNAVVISPRFTSVHQVALNQCICKYGVQGCGLQETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVISPRFTSVHQVALNQCICKYGAQGCGLQETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150
m734.pep	LKK					
g734	LKK					
	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```

a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCCGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTGG CAGGTTAAAA CCACAAAAGA AGATTCGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

```

a734.pep
1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51  KSEAFAELEA FCKGQDTLAG IEDEPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRFTSVYQV ALNQCICKYG AQGCGLQETV YCTSSSYGG
151 TVRSLIQNLK *

```

a734/g734 95.6% identity in 160 aa overlap

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVISPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVISPRFTSVHQV					
	70	80	90	100	110	120
a734.pep	ALNQCICKYGAQGCGLQETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCICKYGAQGCGLQETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

g735.seq not found yet
g735.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

```

m735.seq
1  ATGAATCTCG TGAAGCTGCT GCGCAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG

```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
 51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
 101 KKEIENVLTQ DRKNASGGCI DGFSGHGLQL YNRALGYGN*

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
 51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
 101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
 151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
 201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
 251 TGGCTTTGTC GAAAAACAG GCGGAAGTCA GCCGTCGTAA AACGGAAAAAT
 301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
 351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
 51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
 101 KKEIENVLTQ DRKNAGGGCI DGFHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCCGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCT TCGGTATGGT
 201 TTTGGGTTTG CAGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGGCGGAAC TGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCCG GTGGTTGCCG CGCGTTTTCG GCGGGCGGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTGCGCG GCATTTTCGG
 501 CGCGTATTTG GTCGCGGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCGAGT GCAGAACAA ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTQOLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVING
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTCCGT CGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGGCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
 251 TTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCC CGCGTTTTTG GCGGGCGGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCG GCATTTTCGG
 501 CGCGTATTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAC ATTACGATC ATTACGATG AATCAACGGT
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
 151 FSMPLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHYDVING
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLGLDS					
g736	MKTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCPTSEGILRASTRVVS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGATTGTG TGCCGTTTCA GGGCTGTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TCGCGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTAA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCGAAAT GCAGAACAAC ATCACGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGGCTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTGCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLWLGLDS GIFWSQMNN ITIHYDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPILLASIFNVAGIFGAYLVGVTLWLGLDS					
m736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPILLASIFNVAGIFGAYLVGVTLWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					

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```

m736      GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS
           190      200      210      220      230      240
           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq..
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

m737.pep      10      20      30      40      50      60
               MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAQEAALAR
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737           MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAQEAALAR
               10      20      30      40      50      60
               70      80      90      100     109
m737.pep      VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
               |||||:|||||:|||||:|||||:|||||:|||||:|||||
g737           VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

a737.seq

```

1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAAHQ HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAAHQ	HSKQDKIISR	AQAEKAALAR
m737	MNIKHL	LLTSAAT	ALLSIS	APALAH	HDGHG	DDDHGHAAHQ
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1 ATGTCGCGTG AACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACAGCC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCGCGCC TGATGTCCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGTGTGCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCGCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgt ACCCTGTTTG
401 CCTGGTCCGT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCG CTTCAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTC CTCAGCACCT TGTTACCCCA TTCCCAACAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGC AAAC AGCCCGATGC TGTCTTTT TA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATA CCGCCCTAC TCCGCCACCT

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACA
 1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDA
 51 AAGLIVLLFL TAGKKLFDVK IPAISFLFA MAAFWLQAR LMNLIYPGMN
 101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
 151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
 201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AATIALILPFW YFRSDKSNRR
 251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPROS
 301 EWNKALAAFO SAPIFGHWGN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
 351 IILQLLAEMG ISGTLVVAAT LLTGIAGLLK RSLTPASLFL LCA LAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI IAFKKAANLG ILTASAIIFA
 451 GLLHLDWYTY RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQGVKVAEK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
 601 KPCK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
 51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT
 101 TCGCGCTCAA ACTGAAACCG TCGCCGACT TTTACCACGA TGCCCGCGCC
 151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAAGTGT
 201 TGATGTCAA ATCCCGCCA TCAGCTTCTT TCTGTTTGA ATGGCGCGCT
 251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
 301 GACATCGTCT CTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTG
 351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTT
 401 CCTGGTCTG GCTTATCGGC TCCCTGCTTC AATCTGTCAT CGTCGTCATC
 451 CAGTTTGGCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA
 501 CAGCGGGCAA GCGCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC ACCATCTCTG AAACCTTTAC TGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
 951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
 1001 ACAACATATA CGACAACTC CTCAGCAACT TGTTCAACCA TTCCACAAC
 1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
 1151 CCCCCGATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTTCGG
 1251 ACTGATGCTC TTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
 1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
 1451 TGGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
 1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
 1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
 1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDA

```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFYWLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGS IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTF RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFAPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSYV PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPIIYLPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIIYLPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTFLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTFLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	NLGHYLMWGI LAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	NLGHYLMWGI LAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TILETFTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN AILETFTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TILETFTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN AILETFTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	EWNKALAA FQSAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN IVLQLLAEMG					
g738	EWNKALAA FQSAPIFGHGWN SFAQQTFLIN AEQHTIHDN FLSTLFTHSHN IILQLLAEMG					
	310	320	330	340	350	360
m738.pep	EWNKALAA FQSAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN IVLQLLAEMG					
g738	EWNKALAA FQSAPIFGHGWN SFAQQTFLIN AEQHTIHDN FLSTLFTHSHN IILQLLAEMG					
	310	320	330	340	350	360
m738.pep	ISGTLLVAAT LLTGIAGLLKRPLTPASLFLICTLAVSMCH SMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAAT LLTGIAGLLKRSLTPASLFLCALAVSMCH SMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	ISGTLLVAAT LLTGIAGLLKRPLTPASLFLICTLAVSMCH SMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAAT LLTGIAGLLKRSLTPASLFLCALAVSMCH SMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					
	430	440	450	460	470	480
m738.pep	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSEPLSFYADFSLVNFALPEYPETQTWAEETLKS LKYPHSATYRIALYL					
g738	INELRYISANSEPLSFYADFSLVNFALPEYPETQTWAEETL KALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEP					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

a738.seq

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCGGCC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGTTCCTT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCGGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCCGCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCGGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCCG
1251 ACTGATGCTC TTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCG CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAACT TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCGG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

```

1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLLFL TAGKKLFDVK IPPISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TILGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI
301 EWRKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKQVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

a738.pep	10	20	30	40	50	60
m738	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
m738	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
m738	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
m738	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
m738	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
m738	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
m738	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
m738	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
m738	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLK	DCKAF	AAAPGH	PEA	
m738	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLK	DCKAF	AAAPGH	PEA	
	550	560	570	580	590	600

a738.pep	KPCKX
m738	KPCKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGGCGCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCGGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAACG CCCAAAGAAA ACCATACAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCCATAA GAGATTCTC ACAACCTCT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKENKPFER LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD T PKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGGCGCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCGCAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKENKPFER LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQFADTAQT DRQPDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKENHT KPDTPKNTPP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

```

      10      20      30      40      50      60
m739.pep  MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
m739.pep  EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA
          70      80      90      100     110     120

      130     140     150     160     170
m739.pep  DRQPDAGTQAENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPK-----NHTKPD
          :  : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      ADSLTGTGTAENTLKETPVLPNTNAPHPEPRKETPEKQAQPKETPKETPKENHTKPD
          130     140     150     160     170     180

      180     190
m739.pep  PKNTPPKPHKEILDKLF
          ||||| |||||:|||||
g739      PKNTPAKPHKEILDNLF
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCTCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGCCTAA ACCCATATAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

```

      10      20      30      40      50      60
a739.pep  MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
a739.pep  EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          70      80      90      100     110     120

      130     140     150     160     170     180
a739.pep  DRQPDAGAQ AENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPKETPKENHTKPD
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      DRQPDAGTQAENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
          130     140     150     160     170

```

1204

```

              190
a739.pep      PKNTPPKPKHKEILDNLFx
              |||||
m739          PKNTPPKPKHKEILDKLF
              180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTC TGTTATTCC GATTGTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 TTCGTCTCTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLPHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGIILACEATFLFKFVLFDTIKHH
              |||||
g740           MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIILLIVYLPHYFGAFX
              |||
g740           LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCTCTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLPHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLKFVLFDTIKHH
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLKFVLFDTIKHH
           10      20      30      40      50      60

           70      80      90
a740.pep  LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
m740      LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
           70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCGG GCCCTGATTG
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCGCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHS VVALRIEKN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCATAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AACTTATGG AACCGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCGGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGCGGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCA AGCAGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGGCGC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCGAGCG GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHDKDKL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMLVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQNGNKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---ALILTACSSGGGGVAAADIGAGLADALTAPLDHKDKGLQSLTLDQ				
g741	VNRTTFCCLSLTAGPDSRLQQRGGGGVAAADIGTGLADALTAPLDHKDKGLKSLTLEA				
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLAQAQAEKTY---GNGDSLNTGKLKNDKVSFRDFIRQIEVDGQLITLESGE				
g741	SIPQNGTLTSLAQGAEKTFKAGGKDNSLNTGKLKNDKISRDFVQKIEVDGQTITLASGE				
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRG				
g741	FQIYKQDHSASVALRIEKNPNPKIDSLINQSRFLVSDLGGEHTAFNQLPDG-KAEYHGK				
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYTIDFAAQQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYN				
g741	AFSSDDADGKLTYTIDFAAQQGHGKIEHLKTPEQNVELASAEKKADEKSHAVILGDTRYG				
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKQX				
g741	GEEKGTYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTTCT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCTGCAGG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGCAGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCCGA	GCATTTCAGG	AAGATGGTTG	CGAAACGCCA	GTCAGAATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCGG	TTGAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTGCGCGCCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	GCCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAQ	GAEKTYGNGD	SLNTGKLKND	KVSRFDFIRQ
101	IEVDGQLITL	ESGEFQVYKQ	SHSALTALQT	EQVDSEHSG	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAVISGS	VLYNQAEKGS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLEGGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLEGGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKRRAVIGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQQNGKIEHLKSPELNVDLAAADIKPDGKRRAVIGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATG	GTT	TAC	G	CATT	GCC	G	A	AGCC	GAT	G	CG	GGCG	ACAG	C	GTGT	GCT	TAC
51	TTT	GGG	CGG	C	ATGT	ATC	A	AGAG	TAG	GGA	G	GGT	TCCT	GAT	T	TTTC	GGG	C
101	TTA	TTT	TGC	C	CTGT	GAAA	A	CAGAAA	ACT	G	CCCC	GTT	CAG	T	TTCA	ACG	CCT	
151	GCCT	GCA	ACC	G	GCCT	TTG	C	ACTG	CCG	CGC	A	AAC	ACT	TAT	T	TGGG	GAG	G
201	TTGG	TCG	CGG	G	TTA	AGT	GCC	G	ACAA	TACAA	A	CCT	TTT	CTC	A	GGAT	TCAA	AC
251	ATGT	GTT	TGA	C	CAAC	GTT	G	CAG	CTCA	ATG	C	CGA	AGT	GTC	T	TTAT	ACCA	AG
301	AATG	AAT	CCG	A	ATGC	GA	AGT	G	GGGG	CAG	TTT	T	TTCT	GAAA	A	ACGA	ATAT	GC
351	GGCG	GGT	TTG	T	TCGG	GT	GAG	G	ATGC	GT	AGG	C	TTTT	TG	ACT	G	AAAA	AACG
401	AAGT	CAT	CCC	C	GTC	GAG	CCG	A	AAAG	ATA	AGG	C	CATT	GG	AGAA	A	ACTG	AAAG
451	TATC	GT	GAT	G	AAAC	CG	CAA	A	GGA	TAC	CGG	G	GAG	CG	CAA	A	ACG	ATTT
501	TAAA	AAC	CGT	T	TCG	ATA	A	CTG	CTT	CGA	A	ACAG	TAT	CGC	A	AGCC	GCC	GTG
551	CCGC	AGA	AAC	G	CAA	AG	CGG	T	TTG	ACA	AGT	G	GTAT	GAG	TGA	C	CC	TT
601	CTGG	ACT	TTA	T	TCT	GT	CAAG	G	TTCT	TGG	GGG	G	GAT	CCG	GGG	C	TTG	ATG
651	CAAG	GC	GGAA	A	TTT	GTC	GATA	A	AAG	CC	TTG	C	GAAG	GAG	GGC	A	ATCT	TTA
701	ATGC	GG	CACA	A	ACG	TTT	TCCA	A	AAC	AG	CCT	GT	ATG	ACT	CTC	C	TTTA	ATC
751	AAGG	CT	ACCG	C	CAA	ACC	GACG	A	ATAC	AG	TTAT	A	ATG	CCG	TTG	C	GGCA	TAC
801	AGAC	GAC	CGC	C	CAAT	GGG	GAA	A	TTAA	ACT	TGA	A	CCT	GAC	CGC	A	ACAT	ATG
851	TGTT	CGG	CGG	G	GGAG	CAT	GAT	A	TTCT	TTG	TCG	G	GCT	ATG	CCTA	A	CGGT	GAT
901	AAG	ATAC	GTT	C	CGGA	ATAT	CT	A	AGAA	ATCT	TAC	A	GAAC	CGC	GCT	A	ACAG	AGT
951	TCCG	AAT	ACG	C	GGG	GCA	ACG	C	ACG	GCG	TGTA	A	TGCG	GGA	AGT	A	TGTC	AGG
1001	AGCC	GAC	CGG	C	CGATT	TG	TCG	T	TCT	CCT	TTGG	A	TCAG	G	GGA	A	TAA	GA
1051	GATT	GG	CAGG	G	CGT	AC	GATGA	A	AAA	AGG	CAAC	A	CGT	AC	GTTT	A	ATGC	CGA
1101	ATGC	AGG	AAC	A	GCCA	AGAAAA		A	TAAA	AAC	CGA	A	GCCA	AG	CTC	A	GATG	CCG
1151	GCA	AGC	AGG	T	GTAT	TACT	AT	A	GAC	GA	ATACA	A	GCGG	CAG	CCG	A	GAC	ACG
1201	TATG	TCG	ATG	A	TAT	ATG	AGCT	A	GGAC	GAAAA		A	GGCA	ACA	AGA	A	TTCA	GG
1251	CAAT	CCC	GAC	G	GGC	AC	GCTG	A	CCT	TTAC	CGG	A	TTTT	CCG	GT	A	ACGG	TG
1301	TTT	GGAAA	AAC	A	CGT	CAA	AGTG	A	GCAG	AC	GACC	A	ATGT	CCT	G	A	GCTG	TAA
1351	TACG	CCAA	AAT	A	ACCT	CA	ACAC	A	CAAC	AAA	AAC	A	CATT	CG	CTGA	A	CTGC	CAG
1401	GCGT	TTCA	AC	A	GTA	ACC	GGCC	A	GACT	GC	ACCT	A	TTT	GGG	CGG	A	CTGC	ACTA

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGGTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGGCGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTTCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCGTGCA CATATCCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
  1 MVGIGAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
 51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNATFEQYR SRRAAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGYAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP DGDLS SPLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVMV ADDHVPALYN
451 YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
  1 ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGCACAGCA GTGTGCTTAC
 51 TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTG CTGTGAAAAT CAGAAACTG CCCCGTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTGTC GGCATACCAA
801 AGACGACCGC CAATGGGAA TTAACCTTGA CCTGACCGGC ACATATGGGC
851 TGTTCGGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CCGCGATGAA
901 AAGATACGTT CCGAATATCT GGAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TCGGGGAAGT TGTCAGGGGG
1001 AGCCGGACCG TGATTGTGCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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1201 TATGTCGATG TATATGAAC TGGATGAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCGCT CCTTTACCGG TTTTTCGGT ACAGTGCCGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAAT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACAGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGGCTA TGTTCCTGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGGCGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGAGGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAA
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
1  MVGIAEADA GDSSVLTGG MYQKSREVPD FSGIILSCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101 NESDAKVQGF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAERKAG FDECMASAPFA
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFNR
251 KATANRRYSY MPLRHTKDDR QWGIKDLTG TYGLFGREHD FVGYAYGDE
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGEFDGDL SFLVRGHKEP
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNTNKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNTGADPNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

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a742/m742 98.5% identity in 783 aa overlap

```

a742.pep      10      20      30      40      50      60
MVGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR
|||||
m742          10      20      30      40      50      60
MVGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR
|||||

a742.pep      70      80      90     100     110     120
NTYLGEDWSRSLSDKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVQGFLLKNEHAAGL
|||||
m742          70      80      90     100     110     120
NTYLGEDWSRSLSDKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVQGFLLKNEYAAGL
|||||

a742.pep     130     140     150     160     170     180
SDEDAVGFLTTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR
| |||||
m742         130     140     150     160     170     180
SGEDAVGFLTTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR
|||||

a742.pep     190     200     210     220     230     240
SRRAERKAGFDECMASAPFALDFICQGSWGDGPGVDADKSEFVDKALAKEGIFNNAQRFP

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1210

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|||||:|||||:|||||:|||||:|||||:
m742      SRRRAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240

          250      260      270      280      290      300
a742.pep  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          |||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300

          310      320      330      340      350      360
a742.pep  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360

          370      380      390      400      410      420
a742.pep  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTFVYVDVYELDEKGNKIQTNP
          |||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTFVYVDVYELDEKGNKIQTNP
          370      380      390      400      410      420

          430      440      450      460      470      480
a742.pep  GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTHSLTAGTRFNVTGRLHLLGG
          |||||:|||||:|||||:|||||:|||||:
m742      GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTHSLTAGTRFNVTGRLHLLGG
          430      440      450      460      470      480

          490      500      510      520      530      540
a742.pep  LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540

          550      560      570      580      590      600
a742.pep  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLLQGRNLNASFALFYLEQKNR
          |||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLLQGRNLNASFALFYLEQKNR
          550      560      570      580      590      600

          610      620      630      640      650      660
a742.pep  TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660

          670      680      690      700      710      720
a742.pep  AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720

          730      740      750      760      770      780
a742.pep  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNTRGANNFYGEPRTVSMKLD
          |||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780

a742.pep  WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLLILGARASNYRFDYAL-- 564

Query: 495 PVRVYQGPASDFQTASSIKADQDHYTAKMQGHKLTTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLLQGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAEVAERLAKNTG 674
 S + + +G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IROGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWELTLGGGVNWNKSTLNFAFYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTGANNFYGEPRTVSMKLDWQF 783

RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNIFDKKY----YAGMAGSYGHYGAPRNATVTLRDYF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC
351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
551 TGATCCGTAA GTGA

```

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

```

1 MNQNHFSLSKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSRLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCTG
151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC

```

1212

```

351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTGTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

a743.pep	10	20	30	40	50	60
	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT					
m743	10	20	30	40	50	60
	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
a743.pep	70	80	90	100	110	120
	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHLEEAAMKNTTGVNVVRDSGLQTRFL					
m743	70	80	90	100	110	120
	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHLEEAAMKNTTGVNVVRDSGLQTRFL					
a743.pep	130	140	150	160	170	180
	SRGFYIDQIGEDGITVNVVAGRSGYTAKIDVSPSTDLAVYDHIEVVVRGATGLTQSNSEPGG					
m743	130	140	150	160	170	180
	SRGFYIDQIGEDGMTVNVVAGRSGYTAKIDVSPSTDLAVYDHIEVVVRGATGLTQSNSEPGG					
a743.pep						TVNLIRKR
m743						TVNLIRKX

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTATA CCGAATATTT GTAAAAGGAG
101 AATATTTGGA TGAATTATGT GAACCAAATA TTTGTTTTT AATCGGAGAA
151 AAGGGAAGTG GAAAGACAGC ATATGCTGTT TATTTAATA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTTAATAAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGTATC CTTTGTAGAA CCCAGCAAGA
951 AAAACAAAGT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
1051 AGCTTCCATA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAATACA AAGATCATCT TTTGTTTTAT TATAGTCAA GTGATTATCA
1251 AAATTCCTG AAATTTTGT AATTTTAAA CGGGAAGAT AGATTTAAT

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1213

```

1301 ATAGTGATTT TTTAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAC TGAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
1  MKPLKLTLEFG FVDAANYRRR ENKDLFNRIK VKGEYLDELK EPNISFLIGE
51  KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQQ ITFTESKFOA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNN TKLDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNF KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLQFLF DLNVIAAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
1  ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TGCACTGGG
51  GACAATATTC ATCAATAAGA AAACCTCAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTG TTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTT GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
1  MFVQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
51  ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
1  ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACCAGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCAACA ACCCTGCCT TGAATCCGC CGCGGAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTG GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCAGAAAC TGCTGCCGAA AAAACCAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

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```

751 GCGCAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCGC CTTGAGCCTC CAGCGCAAAA TGAAGCGCGC GGGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAAC
1001 TCGCGTGCAC CGGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

```

g746.pep
1 MSENKQNEVL TGYEQLKRRN RRLVTASSL VAASCILLAA ALSSDPADSN
51 PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPDQ LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEKPKQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAEE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AOKTDRKADK KTAKEKESGK AGKKAATQAG YAEKERALS LQRKMKAAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

```

m746.seq
1 ATGTCGGAAC ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACCTCAA
51 ACGGCGCAAC CGCGCGCGCC TCGTAACGGC AAGTTGCCGT GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGGAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCGGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACCTG CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAGG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACARAAGCGGA CAAGACCAAA
751 ACCGCGGAGA AGGAAAAATC CGGTAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGCGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATT
951 GAACAAATTG CGGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

```

m746.pep
1 MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51 AGETSGVENK AAGAAQTPAL KSAADKPDQL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPEKQAKR AAEKVPATAD
151 STDTVAVEKP KRTAETKPKQ AERTAKAKPK AKETKTAEKV ADKEPTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVV
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```

m746/g746 89.9% identity in 346 aa overlap

          10      20      30      40      50
m746.pep MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT----AGETSG
          |||
g746      MSENKQNEVL TGYEQLKRRN RRLVTASSL VAASCILLAA ALSSDPADSN PAPQAGETGA
          10      20      30      40      50      60

          60      70      80      90     100     109
m746.pep VENKAAGAAQTPALKSAA-----DKPDQLAGEDKPSAADSEISEPENVGAPLVLINER
          :|
g746      TESQTANTAQTPALKSAAENGETAADKPDQLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90     100     110     120

```

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETA KTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
          |||||
g746      LEDSNIKGLEASEKLQQAETA KTAPKQAKQRAAEKVSATADSTDTVAVEKPKRTAETKPQ
          |||||
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAESKKTAEK
          |||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKT KPD TAKSDSAVKEAKKADKAEGKKTAEK
          |||||
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRMKAAGID
          |||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRMKAAGID
          |||||
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||||
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAAACAAA CGAAGTCCTG AGCGGTACG AACAACTCAA
51  ACGGCGCAAC CGCGCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCCGCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCGGCGGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAACCCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGCAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAGTT GCCGACAAAC CGAAAACGTC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAAGCGGA CAAGACCAAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATTG AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CRAAGCACTA TAAAAACGCA AGGGATGCCG AACGCGATTG
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL SGYEQLKRRN RRLVLTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPKQAKOR AAEKVPATAD
151 STDTVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAEEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746: 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCI LLAALSSGPAEQTAGETSGVENK
          |||||
m746      MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCI LLAALSSGPAEQTAGETSGVENK
          |||||
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
a746.pep	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
a746.pep	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
a746.pep	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAAACC
201 CCGTGAGATT GTTTTGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

              10      20      30      40      50      60
a747.pep      LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
              |||||
m747          LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR
              10      20      30      40      50      60

              70      80      90      100
a747.pep      HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
              |||||
m747          HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
              70      80      90      100

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLFDPYYR 60

+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+

Sbjct: 174 INPWSEVKKFDLNSRYKLNTGVNTLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95

+T + E + GD + ++ EYG RV F

Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1  ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51  CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151 CAAGCCTATC CTTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCCGG
201 GCAGGCGGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACACTGA CGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAACTCC CGTCAGCCGG
351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTTACCG
401 TGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501 AAAAAGCTGG TCGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTCACCC
551 CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAACA CACCGCCCAA
601 ACCGCGCTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651 CGCGCGGATG GCGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701 ACCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGC
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAA CAGCGGGGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCTCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCCGCGC GCCTACAGC
1051 TATTCTCGCG GACCCGCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAAAT TTGCCGACGG TTTCACTTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CCGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGGGAAAA GGCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1  MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAQLENLF RTLTARIEFL
101 TQGGEYQDGD DKLPASAGSI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHATAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLQEQTD IFGRRKYSGA
301 PMDGGKKEADG PDFAKDPEGD ITPKDSHMLR ANPRDPEFLK KHCLFRRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG

```

1218

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq
1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAATCATAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CTTCAACCC CGACGGGTTG ACCGTTACCG
401 TGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
701 ACCCAAGTGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGCAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAATAA CAGCGGTGCG
901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATACGCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AAACACCGCC TCTTCGCGC CGCTACAGC
1051 TATTGCGCGG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAAAC TTGCGGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTGCGCGG CGTGGAAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGG GTATAA

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep
1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQQAQ SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGEYQDGD DKLFPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLEQTD IFGRRKYSYA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

m748.pep	10	20	30	40	50	60
	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
g748	MSQNQPAQPT	KRNLFKTAIA	AGAVGAIGGY	FGGKKQGETA	ERTAESQHSP	QAYPCYGEHQ
	10	20	30	40	50	60
m748.pep	70	80	90	100	110	120
	AGIVTPQQAQ	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLFPAGSGI
g748	AGIVTPROAQ	SIMCAFDVTA	QSAKQLENLF	RRTLTARIEFL	TQGEYQDGD	DKLFPAGSGI
	70	80	90	100	110	120
m748.pep	130	140	150	160	170	180
	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLK	DKKPIHLQEM	RDFSNDKLQK	SWCDGDLQLQIC
g748	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLK	DKKTVHLQEM	RDFPNLQKSW	CDGDLQLQIC
	130	140	150	160	170	180
m748.pep	190	200	210	220	230	240
	AFTPETCQAA	LRDIKHTVQT	AVIRWSIDGW	QPKSEPGAMA	AARNLLGFRD	GTGNPKVSDP

	190	200	210	220	230	240
g748	AFTPETCQTALRDIKHTAQTA VIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748.pep	250	260	270	280	290	300
	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDIFGRRKYSGA					
g748	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDIFGRRKYSGA					
	250	260	270	280	290	300
m748.pep	310	320	330	340	350	360
	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ					
g748	PMDGKKEADQPDFAKDPEGDITPKDSHMLANPRDPEFLKKHCLFRRAYSYSRGPASSGQ					
	310	320	330	340	350	360
m748.pep	370	380	390	400	410	420
	LDVGLVFVCYQANLADGFI FVQNLLNGE PLEEYISPFGGGYFFVLPGVKGGFLQGQLLG					
g748	LDVGLVFVCYQANLADGFI FVQNLLNGE PLEEYISPFGGGYFFVLPGVKGGFLQGQLPG					
	370	380	390	400	410	420
m748.pep	VX					
g748	VX					

```

a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCTGGAGCAG TCGCGCGCAAT CGGAGGTTAT CTCGGCGGCA
101  AAAAACGGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151  CAAGCGCTATC TCGTCTACGG CGAACATCGA CGAGGACTCG TTACGCCGCA
201  GCAGGCGTGT TCGATTATGT GCGCTTTCGA CGTAAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCAGCTGTA CCGCCCGCAT CGAGTTTCTC
301  ACCAAGAGCG CGGATATACA AGACCGCGCAC GACAAACTTC CGCCAGCCGG
351  CAGCGGATCT TTGGGCAAGC CTTTCAACCC CGACGGGTTG ACCGTATCCG
401  TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAACCGATTG ATTTGACGGA AATGCGCGCAC TTCTCCAAGC ATAAGCTGCA
501  AAAAAGCTGG TGCAGCAGCG ATTTAGCGCT GCAAATCTGT GCCTTCACCC
551  CGAAACCTGG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601  ACCGCGGTTA TTCGCTGGAG TATFCAGCGG TGGCGACCTA AATCGCAACC
651  CGCGCGGATG GCGGCGCGTGA ACCTGTTGGG CTTCCGCGAC GGCACGGGCA
701  ACCCCAAAGT TTCCGACCCC AAAACTGCCG ACGAGGTTTT GTGACCGGGG
751  GTGGCGCGCA ACAGCTCTCGA GCAACCGGAG TGGCGGAAAA ACGCGAGCTA
801  TCAGGCAGTC CGCCTTATCT GCCACTTTGT TGAGTTTTGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAAAATA CAGCGGCGCG
901  CCGATGCGAGC GCAAAAAGAA AGCCGACCAA CCGGATTTTG CCAAGAACCC
951  CGAGGGGAAT ACCACGCCCA AAGACAGCCA TATACGCTTC GAAATATCCG
1001  GCGATCCCGA GTTCCTTAAA AAACACCGCC TCTTCCGCGC CGCCTACAGC
1051  TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTGC GGCTGTGGTT
1101  CGTCTGCTAT GACCAAAACC TTGCGCAGCG ATTCATCTTC GTGCAAAACC
1151  TCCTCAACGG CGAACCCGCT GAAGAATACA TCAGCCCTTT CGGCGGCGGC
1201  TATTTTCTTC TCTTCCCGCG CGTGGA AAAA GCGCGCTTTT TGGGCAAAAG
1251  GCTGCTGGGC GTATAA

```

```
a748.pep
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQA F SIMCAFDVTA QSAKQLENLF RDLTARIEFL
101 TQGGEYQDGD DLKPPAGSGI LGKAFNPDL TVTVVGSSL DDFGRFLKDL
151 KPIHQLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGM AARNLLGFRD DTGNPKVSDP KTADEVLTVM
251 VAANSIDLEPE WAKNGSYQAV RLRIHFVEVF DRTLQEOGT IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEG TTPKDSHIRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSQG LDVGLVFVCY QANLADGFIF VQNLNLEPL EEEYISPFGGG
401 YFFVLPGVEK GGFGLGGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

```

a748.pep      10      20      30      40      50      60
MSKNQPAQPTRRRLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSPPQAYPCYGEHQ
|||||
m748          10      20      30      40      50      60
MSKKQPAQPTRRRLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPPQAYPCYGEHQ
|||||

a748.pep      70      80      90     100     110     120
AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI
|||||
m748          70      80      90     100     110     120
AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI
|||||

a748.pep     130     140     150     160     170     180
LGKAFNPDGLTIVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDLSQLIC
|||||
m748        130     140     150     160     170     180
LGKAFNPDGLTIVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDLSQLIC
|||||

a748.pep     190     200     210     220     230     240
AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
|||||
m748        190     200     210     220     230     240
AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
|||||

a748.pep     250     260     270     280     290     300
KTADEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSYA
|||||
m748        250     260     270     280     290     300
KTADEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDFGRRKYSYA
|||||

a748.pep     310     320     330     340     350     360
PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
|||||
m748        310     320     330     340     350     360
PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
|||||

a748.pep     370     380     390     400     410     420
LDVGLVFCYQANLADGFIFVQNLLNGEPLLEYISPFGGGYFFVLPGVKGGFLGQGLLG
|||||
m748        370     380     390     400     410     420
LDVGLVFCYQANLADGFIFVQNLLNGEPLLEYISPFGGGYFFVLPGVKGGFLGQGLLG
|||||

a748.pep      VX
||
m748          VX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

```

g749.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGCCGGAGAA AGCCGCGCCG GCCCGCTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGT GAATCTGACC GTGCCGAGCG GACAGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAaccct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTC AAGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT
551 CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGTGTG AAGACGACTT
651 CAAAGACGGT GCGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACCGCGGCC
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAATCG ACGCATTGGC

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1221

```

801 GttccctCCG GGCAGAGTGG TCGCGGCGCG GTCCGAACTG ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGCGA TCTAAAAAAA TCGTCGATT
951 GTTCGGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGACCAAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGGCGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLIALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIIVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSQVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAATAT CGCGTCAAC
151 GACAAATGCTT GCGAACCGAT GGAAGTACG GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCTCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCG CGGACTTTCC
301 GATAAATGA CCGTCAACCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAC
501 CAAACTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCTCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAATGATGA CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTCTCTCCG GGCAGAGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATT
951 GTTCGCTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGGCGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLIALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIIVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSQVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNLIALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT
          |||
g749      MRKFNLIALSVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIIVNDNACEPMNLT
          10      20      30      40      50      60

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	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNN	SGRKLEWEILK	GMVVD	ERENIAPGL	SDKMTVTL	LPGEYEMTCGLLT
g749	VPSGQVVFNIKNN	SGRKLEWEILK	GMVVD	ERENIAPGL	SDKMTVTL	LPGEYEMTCGLLT
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD	SGFKDTANEAD	LEKLSQPLADY	KAYVQGEVKEL	VAKTKTFTEAV	KAGDIE
g749	NPRGKLVVTD	SGFKDTANEAD	LEKLPQPLADY	KAYVQGEVKEL	AAKTKTFTEAV	KAGDIE
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRV	HYERIEPIAE	LFSELD	PVIDAREDD	FDGAKDAGFT	GFHRIEYALWVEK
g749	KAKSLFAATR	VHYERIEPIA	ELFSELD	PVIDACEDD	FDGAKDAGFT	GFHRIEHALWVEK
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAK	LMTDVEALQ	KEIDALAF	PPGKVVG	GASELIEE	VAGSKISGEEDRYSH
g749	DVSGVKETA	AAKLT	DVEALQ	KEIDALAF	PPGKVVG	GASELIEE
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDG	SKKIVDLFR	PLIEAKNK	ALLEKTD	TNFKQVNEI	LAKYRTKDG
g749	LSDFQANADG	SKKIVDLFR	PLIEAKNK	ALLEKTD	TNFKQVNEI	LAKYRTKDG
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKA	LQASIN	ALAEDLA	QLRGILGLKX		
g749	EADRKA	LQAPIN	ALAEDLA	QLRGILGLKX		
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

```

a749.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCCGCTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAAATGCC TCGGAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGGCG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGCG GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAGAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCTG AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAATA CCGGACTAAA
1051 GACGTTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGCGA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

```

a749.pep
1  MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFDKG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVVGASEL IEEVAGSKIS GEEDRYSHTD

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301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLKX*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	MRKFNLTALSVMLALGLTACQPPEAEKRAAPASGEAQTANEGGSVSI	10	20	30	40	50	60
m749	MRKFNLTALSVMLALGLTACQPPEAEKRAAPASGEAQTANEGGSVSI	10	20	30	40	50	60
a749.pep	VPSGQVVFNIKNNSGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	70	80	90	100	110	120
m749	VPSGQVVFNIKNNSGRKLWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	70	80	90	100	110	120
a749.pep	NPRGKLVVTDGSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	130	140	150	160	170	180
m749	NPRGKLVVTDGSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	130	140	150	160	170	180
a749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	190	200	210	220	230	240
m749	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	190	200	210	220	230	240
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD	250	260	270	280	290	300
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD	250	260	270	280	290	300
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG	310	320	330	340	350	360
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG	310	320	330	340	350	360
a749.pep	EADRKALQASINALAEDLAQLRGLGLKX	370	380	389			
m749	EADRKALQASINALAEDLAQLRGLGLKX	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq
 1 GTGAAACCGC GTTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCCTG
 51 TTCGCCCCGAA CCTGCCGCCG AAAAACTGT ATccgCCGCA TCCCAAGCCG
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
 151 GTTGTGCCGA AGAATCCCGA ACgcgctcgcc gtgtAcgaCt ggCGGCGTt
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCCGCCCGG
 251 TGC GCGTGA CTATTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
 301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
 351 TGTCATTACC GGC GGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
 451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGTA AGGAAGCGCG
 501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
 551 AAGCCGCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACAGGCAAC
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
 651 CGACATCGGC CTGCCGCCG TGGACGAATC TTTACGCAAC GAAGGGCACG
 701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
 751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

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801 GGAAGTGTG GATAACGCGC TGGTATGCGG CACGAACGCT TGAAGCGCA
 851 AGCAAATCAT CGTCATGCCT GCGCGGAAC ACATTGTCGC GGGCGGCGCG
 901 CCGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
 951 AGAACCCGTT GCGGCGCAGT AG

This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:

g750.pep

1 VKPRFYWAAC AVLEAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
 51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLO PAFDKAATVG
 101 TLFEPDCESL HRHNPQFVIT GPGAEAYEQ LAKNATTIDL TVDNGNIRTS
 151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKKGK RGLVLSVTGN
 201 KVSAGTQSR LASWIHGDIG LPPVDESLRN EGHGQPVSE YIKEKNPGWI
 251 FIIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
 301 RQLIQAAEQL KAAFEKAEPV AAQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2575>:

m750.seq

1 GTGAACCCGC GTTTTATTG GGCAGCCTGC GCCGTCTGCG TGACCGCCTG
 51 TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
 101 CCGCCACGCT GACCGTGCCG ACCGCGCGGG GCGATGCCCT TGTGCCGAAG
 151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
 201 CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
 251 ATTTGCAGCC TGCATTGTAC AAGCGCGCAA CGGTGGGAC GCTGTTGAG
 301 CCCGATTACG AAGCCCTGCA CCGCTACAA CTCTAGCTTG TCATTACCGG
 351 CCGGCGCGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCAACA
 401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
 451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
 501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAG
 551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
 601 TTCGGCAGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
 651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
 701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
 751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
 801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
 851 TCATGCTGCG CGCGAATAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
 901 CAGGCGCGCG AGCAGTTGAA GCGGCGGTTT AAAAAGGCAG AACCCGTTGC
 951 GCGGGGAAA AAGTAG

This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:

m750.pep

1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
 51 NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
 101 PDYEALHRYN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
 151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
 201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSFEYIKE KNPDWIFIID
 251 RTAAIQEGEP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
 301 QAAEQLKAFF KKAEPVAAK K*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSPEPAAEKTVSASASASAAAAATLTVPTARGDAVVPKNPERVA				
g750	VKPRFYWAACAVLPAACSPEPAAEKTVSASQAASTPVATLTVPTARGDAVVPKNPERVA				
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLEFDPDYEALHRYNPQLVIT				
g750	VYDWAALDTLTEPGVNVGATTAPVRVDYLQPAFDKAATVGTLEFDPDCESLHRHNPQFVIT				
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFA				

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```

g750      GGPGEAEYEQ LAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
          130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
QTREAAKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIPLPPVDESLRNEGHGQPVSF
g750      QKREAAKGRGLVLSVTGNKVSFAFGTQSRLASWIHGDIPLPPVDESLRNEGHGQPVSF
          190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGA
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVCGTNAWKRKQIIVMPAANYIVAGGA
          250      260      270      280      290      300

m750.pep  300      310      320
RQLIQAAEQ LKA AFKKAEPVAAAGKKX
          310      320
g750      RQLIQAAEQ LKA AFKKAEPVAAQX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1   GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCGCAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACACT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGAC AAGCGGCGAA CGGTGGGGAC GCTGTTGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT GCGGAAAAAC GCGACCAACA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTGCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGCAACAA GGTGTCGCC
601 TTCGCACGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751 CGTACCGCGC CCATCGGGCA GGAAGGCGCG GCGGCTGTG AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAATCATCG
851 TCATGCCTGC CGCGAATAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901 CAGGCGCGCG AGCAGTTGAA GGAGGCGTTT GAAAAGCAG AACCCGTTG
951 GCGGGGAAA GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1   VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAO IDALFAQTR EAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIPLPPV DESLRNEGHG QPVSFYEIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVDNAL VRGTNAWKRK QIIVMPAANY IVAGGSRQLI
301 QAAEQ LKEAF EKAEPVAAAG E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

```

a750.pep  10      20      30      40      50      60
VKPRFYWAACAVLLTACSPEPAAEKTVSAA S A S A A T L T V P T A R G D A V V P K N P E R V A V Y D W
|||||
m750      10      20      30      40      50      60
VKPRFYWAACAVLLTACSPEPAAEKTVSAA S A S A A T L T V P T A R G D A V V P K N P E R V A V Y D W
|||||

a750.pep  70      80      90      100     110     120
AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYN POLVITGGPG
|||||
m750      70      80      90      100     110     120
AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYN POLVITGGPG
|||||

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	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNI RTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNI RTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
a750.pep	190	200	210	220	230	240
	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWINGDIGLPPVDES LRNEGHGQPV SF EYIKE					
m750	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWINGDIGLPPVDES LRNEGHGQPV SF EYIKE					
	190	200	210	220	230	240
a750.pep	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWK RKQIIVMPAANYIVAGGS RQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWK RKQIIVMPAANYIVAGGARQLI					
	250	260	270	280	290	300
a750.pep	310	320				
	QAAEQLKEAFKAE PVAAGKEX					
m750	QAAEQLKAAFKAE PVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

```
m751.seq..
1  ATGGCTTGA  GTATGTTTGC  CACAACCCAA  GCCGATAGAG  CGGTAAGGTC
51  TGCAACTGCA  CCTAAAGAAA  TGTGGTTCCA  TAAGAAGATA  ATAGATGAAA
101 AAACAGGTAA  AGTATCCTTT  GATACCAGAC  AAATTGGTGC  ATTGAATGAT
151 TTAAGCAAGG  AAGAACTGGC  AAGCATTCAA  GACACAAATG  GCAAAGTTAT
201 TACTGTGTCT  AATCCTGGTA  TTTTCAATAA  TCGAGAAGAT  TCATTAAGCA
251 ACGCAGCAAA  ACAAATCGT  AATAGTACAA  ACGGTAGTGG  TGTATTGCA
301 GTCATGAATC  CTCCAACAGG  GAAATATAAA  TCTGATTCTA  ATAACAAAAT
351 AAAAGATTTC  TTATGGCTCG  GTTCAAGTCT  TGTTCCTGAA  CTGATGTATG
401 TCGGTTACGA  CCAATTAAAT  AATAAAGTGT  TCCAAGGCTA  TTTACCCAAA
451 ACCAATTCAG  AAAAATGAA  TCAAGATATT  TATCGAGAGG  TTCAAAAAT
501 GGGTAACGGC  TGGTCGGTTG  ATACCAGTAA  TCACAGTCGT  GGGGGAATTA
551 CAGCAAGCGT  TTCCTTAAAA  GATTGGGTAA  ACAATCAAAA  ACAAATGGC
601 ATTGCCCCAA  TCAGAAAAGC  ACGTTTCTAT  GGTACAGCCA  CAAATGTGCA
651 GAATGATTAC  GCCGATGTTT  TACAGAAAAA  CGGCTATACC  TATACGGGTG
701 CAGACGGCAA  AACTTATAAC  AGCGATCCT  ACTCAATCGT  GCATGATAAA
751 GATTTTGTGG  GGAACAAATG  GATACCTTTC  TTGCTAGGAA  CCAATGACAC
801 CACACAAGGT  ACATGTAAGG  GGTGTGCTA  TTGCTAGGAA  AGTTATTTG
851 CGGAGGTGCC  AAAAGCAGGT  ACAAAGAAT  TTGATGACTA  TGTAAAAATA
901 TGGGGTGAAG  TTGAATATGA  CGCTCAAGGT  AAGCCAATTA  ACAAATCTAA
951 ACCCTACTG  GTAGAACCAA  ACAAACAAA  AGATAATGAA  AAATATGAAA
1001 AAGAAGCTTT  CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

```
m751.pep..
1  MAWSMFATTQ  ADRAVRSATA  PKEMWFHKKI  IDEKTGKVSF  DTRQIWSLND
51  LSKEELASIQ  DTNGKVITVS  NPGIFNNRED  SLSNAAKQNR  NSTNGSGVIA
101 VMNPPTGKYK  SDSNNKIKDF  LWLGSSLVSE  LMYVGVDQLN  NKVFQGYLPK
151 TNSEKLNQDI  YREVQKMGNG  WSVDTSNHSR  GGITASVSLK  DWVNNQKQNG
201 IAPIRKARFY  GTATNVQNDY  ADVLQKNGYT  YTGADGKTYN  SGSYSIVHDK
251 DFGVGNKWIPF  LLGTNDTTQG  TCKGLCYSHS  SYFAEVPKAG  TKEFDDYVKI
301 WGEVEYDAQG  KPINKSKPIL  VEPNKTONE  KYEKEAF*
```

a751.seq not found yet

a751.pep not found yet

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g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAAGATTG
601 AAAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAATATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTGCAATTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTC GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCTTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1 MKISRPEFT LLQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFFP
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAAGATTG
601 AAAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC

```

1228

```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGCTCT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCTAGT GCCGTTCAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGAAAGGTT
1401 AAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EQQWFNCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQALE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGVQHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHFPD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVFPK
451 SGNALFYVAP QDLLERLEK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTTCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIT WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSQOM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

1229

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTTCG TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTGCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTTCG CTGACACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```

m754.pep
1  MMKSILTVSG NRMKPRITY LDVWANDERI GTLEKGAMYP FAYDNPSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLESDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKITY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCA
101 TCTTGGCTAG ACATGGATTG GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGTAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGCTGATG AGCAAATCAA TCAGGTTCTG GAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA

```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA LVS DGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGACG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA LVS DGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

```

              70      80      90      100      110      120
m756.pep      TLVRFRGRDMLQDMPPKIRSATLVALTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              |||||
a756          TLVRFRGRDMLQDMPPKIRSATLVALTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              70      80      90      100      110      120

              130      140      150      160      170      180
m756.pep      RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              |||||
a756          RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              130      140      150      160      170      180

m756.pep      LSDIGDX
              |||||
a756          LSDIGDX

```

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51 TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTGAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAOQ QEQAQSELKT MPVSYTDYQS
51 AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGGTGAATTT CCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTCGGTGC GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGGCG TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAAAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGGAAATT CCCGCTCTGCT ACGGCGGCGA ATACGGCCCG
151  GATTTGCGCG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTCCGAG CCGATTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758						
	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
a758						
	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELPFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758						
	130	140	150	160		
	GVYPFASPGGWQIIGRTELPFRADLNPPPTLLAAGDQVRFVAERIEPX					

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCTG CTTACTCATC CATGTGCCG AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGCGC GTTCACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA
 651 AAACCCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTCGACAAAG
 751 CATGAAAACC GCTGGGTGCT TCGGGGCGTA CTCAGCACCT ACGCCGGCTT
 801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT
 851 CCACCATCCG CCAATACGAA ACCCGGTGG ATGTGGGGCT GACCACCAAC
 901 GAACTCATAT GGC CGCAGCAA CGGTAATGGC AACAGCACCC TGCAAGGGCT
 951 CAACGAACGC ATCACCCTGC CCATTGCAA CCCTTCGCTT GCCCACAAA
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA
 1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTACCCGTC GTCGGTAAAA
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA
 1451 GGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTGCG
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA
 1651 TACATCAACC CGCACCGBAA CCGTCGGACC GACTACTTCA TACTCAAACC
 1701 CGCGCGCAAC CCGCGCAAT TTTTCCGTT AAATATGAAA AACTCAACAA
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCGA ACAAGTCGCC
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA
 2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCGTACCC
 2101 CATGCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG
 2151 GACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCC
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA
 2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG
 2351 TTTTAAAAGC CGAAAACATAT CGTGCACTAC CTGCAACGCA AGTACGCGGC
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGCGC ACTGACGCTT
 2551 GACGGCGCAC AAATTACCCT GAACCCGAT TTCGCCAATA ATACACACAA
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC
 2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC
 2751 CGGACAAGAA CCTCAACAA CCGAATCGCT TGCACTTGTC AGCCTCAATC
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACACG GATACAGCCT
 2901 GTACAACCCG CTCAAAGAGG CCGAATCTCA AATTGAAGCC ACGCGTGCAG
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG
 3151 CGTGCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG
 3201 TCAGGTTGCC AAAGCCGCGC ACACGAACGA CCGTACACTC TTCGAAACCG
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC
 3301 AAAGCACGGC AAGGCGGCGA TGCGCAAGCC GTCGAAACAG CCCGGCAGC
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAATC GATCAGCCGG
 3451 TCGGCCAACA CGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGCGA
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA
 3551 ACATCTGGCT GGAACCCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA
 3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC
 3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCGC CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCCTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1  MRFTHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGFTV
51  GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREPYFVR LSGSTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQND SRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FQVSNPKGD RLSKLGA GTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPOGNAAYVE
551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LNGEV LIEGG NMIVSGRPVE
701 HAYDHOAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTL S QSHTGALTL
851 DGAQITLNP FANNTHNNRF NTLTVNGTLD GFGTFRFLTG IVRQNAPPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAE LISR
1151 SANTAVSEQA AYNTGRQOAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQA AHGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1  AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGGC TGATGGAAGG
51  CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGATGTC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1  NNRNTRYAAL GKRVMGVE T EISGAITPKW QIHAGYSYLH SQIKTAANPR
51  DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHY YAR VGGTNTFNIP GSERSLTANL
151 RYSF*

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1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCACT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CCGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCAACC TGTTGCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCC GCAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GAGCGCGGCT ATCTTTACCA GCAACGCCGC CTCGCGCGGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGAC ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGGC GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGG CTTTGCCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAATTTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGAT TGGGCAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTTCG GCGACGAAGG CATCTTCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGTTTCGGA GCGCAGCCTG
2101 ACGGCAAACC TGCCTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTF GSKLNNTGQA DVAGLGTDIK
351 QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVALLD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPCLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
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1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYFYMKDKNAAPLDSNNKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYARVGSESTFNIPGSERSLTANL					
g760	AGMHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYARVGGTNTFNIPGSERSLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSFX					
g760	RYSFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

```

m761.seq
1  ATGAAATAT  CATTTCATTT  AGCTTTATTA  CCCACGCTGA  TTATTGCTTC
51  CTTCCTGTT  GCTGCCGCCG  ATACGCAGGA  CAATGGTGAA  CATTACACCG
101 CCACTCTGCC  CACCGTTTCC  GTGGTCGGAC  AGTCCGACAC  CAGCGTACTC
151 AAAGGCTACA  TCAACTACGA  CGAAGCCGCC  GTTACCCGCA  ACGGACAGCT
201 CATCAAAGAA  ACGCCGCAAA  CCATCGATAC  GCTCAATATC  CAGAAAAACA
251 AAAATTACGG  TACGAACGAT  TTGAGTTCCA  TCCTCGAAGG  CAATGCCGGC
301 ATCGACGCTG  CCTACGATAT  GCGCGGTGAA  AGCATTTTCC  TGCGCGGTTT
351 TCAAGCCGAC  GCATCCGATA  TTTACCGCGA  CGGCGTGCGC  GAAAGCGGAC
401 AAGTGCGCCG  CAGTACTGCC  AACATCGAGC  GCGTGGAAAT  CCTGAAAGGC
451 CCGTCTTCCG  TGCTTTACGG  CCGCACCAAC  GGCGGCGGCG  TCATCAACAT
501 GGTCAGCAAA  TACGCCAACT  TCAACAAAG  CCGCAACATC  GGAGCGGTTT
551 ACGGCTCATG  GGCAAACCGC  AGCCTGAATA  TGGACATTAA  CGAAGTGCTG
601 AACAAAACG  TCGCCATCCG  TCTCACCAGC  GAAGTCGGGC  GCGCCAATTC
651 GTTCCGCAGC  GGCATAGACA  GCAAAATGT  CATGGTTTCG  CCCAGCATTG
701 CCGTCAAAC  CGACAACGGC  TTGAAGTGGA  CGGGGCAATA  CACCTACGAC
751 AATGTGGAGC  GCACGCCCGA  CCGCAGTCCG  ACCAAGTCCG  TGTACGACCG
801 CTTCCGACTG  CCTTACCGCA  TGGGGTTCGC  CCACCGGAAC  GATTTTGTCA
851 AAGACAAGCT  GCAAGTTTGG  CGTTCGACC  TTGAATACGC  CTCAACGAC
901 AAATGGCGTG  CCCAATGGCA  GCTCGCCAC  CGCACGGCGG  CGCAGGATTT
951 TGATCATTTT  TATGCAGGCA  GCGAAAATGG  CAACTTAATC  AAACGTAAC
1001 ACGCCTGGCA  GCAGACCGAC  AACAAAACCC  TGTCGTCCAA  CTTAACGCTC
1051 AACGGCGACT  ACACCATCGG  CCGTTTGTAA  AACCACCTGA  CCGTAGGCAT
1101 GGATTACAGC  CGCGAACACC  GCAACCCGAC  ATTGGGTTTC  AGCAGCGCCT
1151 TTTCCGCCTC  CATCAACCCC  TACGACCGCG  CAAGCTGGCC  GGCTTCGGGC
1201 AGATTGCAGC  CTATTCTGAC  CCAAAACCGC  CACAAAGCCG  ACTCCTACGG
1251 CATCTTTGTG  CAAAACATCT  TCTCCGCCAC  GCCCGATTG  AAATTCGTCC
1301 TCGGCGGCCG  TTACGACAAA  TACACCTTTA  ATTCCGAAAA  CAAACTCACC
1351 GGCAGCAGCC  GCCAATACAG  CGGACACTCG  TTCAGCCCCA  ACATCGGCGC
1401 AGTGTGGAAC  ATCAATCCCG  TCCACACACT  TTACGCCTCG  TATAACAAAG
1451 GCTTCGCGCC  TTATGGCGGA  CGCGGCGGCT  ATTTGAGCAT  CGATACGTTG
1501 TCTTCCGCCG  TGTTCACGCG  CGACCCCGAG  TACACCCGCC  AATACGAAAC
1551 CGGCGTGAAA  AGCAGTTGGC  TGGACGACCG  CCTCAGCACT  ACGTTGTCTG
1601 CCTACCAAT  CGAACGCTTC  AATATCCGCT  ACCGCCCGCA  TCCAAAAAAC
1651 AACCTTATA  TTTATGCGGT  TAGCGGCAAA  CACCGTTTCG  GCGGCGTGGA

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1237

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIIASFPV AAADTDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFARHN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLTL
351 NGDYITIGREF NHLTVGMDYS REHRNPTLGF SSAFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAPIYG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRDPKPN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPGYTARVN
701 YRF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAAT CCTGAAAGGT
451 CCGTCTCTCC TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT
501 GGTACAGCAA TACGCCAACT TCAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCTGT GGCAAAACGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAAC TACGACCGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG GTTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTC TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAATC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCTGTC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGCG CAGCCCGGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCG CCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIIDLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQTYD
251 NVERTPDRSP TKSVDYRFLG PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HSRGVELSA IGQIIPKKLY LRGLSLVMA QVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIIDLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIIDLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVS K YANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRTNGGGVINMVS K YANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQTYTDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVW RSDLEYAFND					
a761	LKWTGQTYTDNVERTPDRSPTKSVYDRFGLPYRMGFAHRNDFVKDKLQVW RSDLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHR TAAQDFDHFYAGSENGNLIK RNYAQQTND NKTLSNLT L NGDYTIGRFE					
a761	KWRAQWQLAHR TAAQDFDHFYAGSENGNLIK RNYAQQTND NKTLSNLT L NGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
|||||
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
              370      380      390      400      410      420

              430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
|||||
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
              430      440      450      460      470      480

              490      500      510      520      530      540
m761.pep  YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTSLAYQIERF
|||||
a761      YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTSLAYQIERF
              490      500      510      520      530      540

              550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
|||||
a761      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
              550      560      570      580      590      600

              610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSRNEKVTTLPGFARVDAM
|||||
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNEKVTTLPGFARVDAM
              610      620      630      640      650      660

              670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDMPGNPRGYTARVNYRFX
|||||
a761      LGWNHKNVNVTFAAANLFNQKYWRSDMPGNPRGYTARVNYRFX
              670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGAG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1   MKWLLNMIMR PIKFSMVNTL LFIVICSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLEFIENFV TKSIYMAIIY PILYFFTICK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAACGGAG CCTTACATT TATACATCCC TATTATTATT AATTTTCT
 401 CACTTTTAGT TTCTAATTT ATTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIIYMAIIY PILYFTIKK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NEFSLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 CGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTC AAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACATAA
 1251 CGGCATCCGC AACCAGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACGG TATTTGCGGA
 1401 ATAA

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This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

```
m763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFAQSHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYGYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

```
a763.seq
1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGCTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCTTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT TTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAATT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGCGAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAGAGAG CGGGTTAGGG TTGGAAACGG TATTGCGGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

```
a763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFAQSHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGOALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHAEAA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYGYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

	10	20	30	40	50	60
m763.pep	MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
a763	MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQ	RD	AVR	RARQQQAKA	AF	LPHV
a763	LPEAWRAAQHSADFQASHYQ	RD	AVR	RARQQQAKA	AF	LPHV
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLF	DAAKFAQYRQ	S	RFD	TQAAEQ	RFD
a763	GWSVQVGQTLF	DAAKFAQYRQ	S	RFD	TQAAEQ	RFD
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQV	RQAQALFN	KGAAT	ALDI	HEAKAGY	DNALAQEI
a763	HAAEKEAYAQQV	RQAQALFN	KGAAT	ALDI	HEAKAGY	DNALAQEI
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAID	TANLLARYL	PKLERY	SLDEW	QRIALS	SNNHEY
a763	TGLDSKQIEAID	TANLLARYL	PKLERY	SLDEW	QRIALS	SNNHEY
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAH	VGYN	LNLYT	SSAQ	NNDYH	YRGK
a763	QNSRYPTVSAH	VGYN	LNLYT	SSAQ	NNDYH	YRGK
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLT	ATERHIK	LAVRQ	AYTES	GAA	RYQIM
a763	QYGAAEAQLT	ATERHIK	LAVRQ	AYTES	GAA	RYQIM
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQ	EVAQAEQ	KLAQ	ARYK	FMLAY	LRLV
a763	NRLEVIRARQ	EVAQAEQ	KLAQ	ARYK	FMLAY	LRLV
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```
m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCGGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGTACAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG GCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAACT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGACGAA AGCTTTAGGG AGCGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```
m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDQHVHKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPFHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVGAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRQOTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```
a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCCTACAC TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CCGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1  MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAF LPAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVS GGRSKTIQPLETAVVKAVHV RDGQHVKGGE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVS GGRSKTIQPLETAVVKAVHV RDGQHVKGGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m764.pep	TLAELEAVGT DSDVVQSEQA LQAAQLSKLRYEAVLAALES RTVPHIDMAQ ARSLGLSDAD					
a764	TLAELEAVGT DSDVVQSEQA LQAAQLSKLRYEAVLAALES RTVPHIDMAQ ARSLGLSDAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m764.pep	VQSAQVLAQH QYQAWAAQDA QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDA QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m764.pep	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m764.pep	LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSPADGTVQELAT YTVGGVVQAA QKMMVIAPDD					
a764	LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSPADGTVQELAT YTVGGVVQAA QKMMVVAPDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m764.pep	DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG KVKSVDHDAV SHEQLGLVYT					

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|||||
a764      DKMDVEVLVLNKKDIGFVEQGDVAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
           370      380      390      400      410      420

           430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
           |||||
a764      AVVSLDKHTLNIDGK
           430
```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1  ATGTTAAGAT GCGGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTTACGGT CATGATTCGG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACACAC TCCAGAACAG CCCGAGGGT GCAGGCAGTA
301 TTTGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG TGGAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGCGCGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```
m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVVG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDEIAAI MGHMETHALH EHGKNKVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEAA DEGGMMLMAQ AGYHPAAAVR
251 VWEKNQEND QNGFIYATTS THPTNNARIE NLKRLLEPTVM PVYEQSVRNK
301 GRVNRKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1  ATGTTAAGAT GCGGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACGGG TCGTTGCTGA TGTTTACGGT CAGGATTCGG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG CGGAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAAACGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```
a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
```

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```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRLPYADA ANNTGKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHETHALH EHGKKNVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLLEEA DEGGMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLPTVM PVYEHVSRNK
301 GRVKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPSVLDSDGIFLKFNF	LRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG				
a765	MLRCRPSVLDSDGIFLKFNF	LRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG				
	10	20	30	40	50	60
m765.pep	70	80	90	100	110	120
	HDSATMNAAAAKDYMKTVELNKSAGNVDTT	SRTARRVQAVFRRLPYADAANNTSHKFDW				
a765	QDSATMNAAAAKDYMKTVELNKSAGNVDTT	SKTARRVQAVFRRLPYADAANNTGKFDW				
	70	80	90	100	110	120
m765.pep	130	140	150	160	170	180
	KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKNKVGQK					
a765	KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKNKVGQK					
	130	140	150	160	170	180
m765.pep	190	200	210	220	230	240
	ILNTAAQIGTQIILDKKPD	TNPVLVGLGMDILGTYGLTLPYSRSLLEEADEGGMLMAQ				
a765	ILTNMAAQIGTQIILDKKPD	TNPVLVGLGMDILGMYGITLPYSRSLLEEADEGGMLMAQ				
	190	200	210	220	230	240
m765.pep	250	260	270	280	290	300
	AGYHPAAAVRVWEKMNQENDQNGFIYAITS	THPTNNARIENLKRLPTVMPVYEQSVRNK				
a765	AGYHPAAAVRVWEKMNQENDQNGFIYAITS	THPTNNARIENLKRLPTVMPVYEHVSRNK				
	250	260	270	280	290	300
m765.pep	310					
	GRVKNKRRRX					
a765	GRVKNKRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAAATG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTACGAACA
351 AAAAATCCGT TTGGAAACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQF GKIEVLEFFG
51  YFCVHCHHFD PLLLLKGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSAV FKAVYEQKIR LENRAVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAVALKMQK LTEQYIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTCTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAACTGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CCGCTGCCGT CAATTTGTCG
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCTATGA TTCCCCGAA
 451 GCTGCCCGCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
 501 CGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAGAATT GGTGCAAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
 51 YFCVCHHFD PLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAVNLS
 101 GLKYQANPAV FKAVYEQKIR LENRSVAGKW ALSQKGFDDG KLMRAYDSPE
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVCHHFD
m767						
	10	20	30	40	50	60
g767.pep	PLLLKLKAL	PSDYLRT	EHVVWRPE	MLGLARMA	AAVKLSGL	KYQANS
m767	PLLLKLKAL	PSDAYLR	TEHVWQPE	MLGLARMA	AAVNLSGL	KYQANPA
	70	80	90	100	110	120
g767.pep	LENRAVAGK	WALSQKGF	DGKKLMRA	YDSPEAAA	VALKMQKL	TEQYIDST
m767	LENRSVAGK	WALSQKGF	DGKKLMRA	YDSPEAAA	ALKMQKL	TEQYRIDST
	130	140	150	160	170	180
g767.pep	PTVIVGGKYR	VIFNNGFD	GGVHTIKEL	VAKVREER	KRQTPAVQ	KX
m767	PTVIVGGKYR	VIFNNGFD	GGVHTIKEL	VAKVREER	KRQTPAVQ	KX
	190	200	210			
g767.pep	VIFNNGFD	GGVHTIKEL	VAKVREER	KRQTPAVQ	KX	
m767	VIFNNGFD	GGVHTIKEL	VAKVREER	KRQTPAVQ	KX	
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
 101 CCATTCCCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
 151 TATTCTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATGGG
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
 251 AGCCTGAAAT GCTCGGCTCG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
 351 AAAAATCCGC TTGGAACA GGTGCGTTGC CGAATAATGG GCTTTGTCTC
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCTACGA CTCTCCTGCG

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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
 501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
 551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

a767.pep
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
 51 YFCVCHHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
 151 AAAAASKMQQ LTEQYRIDST PTVVVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVCHHHFD					
m767	MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVCHHHFD					
	10	20	30	40	50	60
a767.pep	PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR					
m767	PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR					
	70	80	90	100	110	120
a767.pep	LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGGKYR					
m767	LENRSVAGKWALSQKGFDDGKLMRAYDSPAAAAALKMQKLTQYRIDSTPTVIVGGKYR					
	130	140	150	160	170	180
a767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

g768.seq
 1 ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTACGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAATGA

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

g768.pep
 1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNIPI VDQIVRRIYE AAPDKDTPVN LYCRSGRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGMK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

m768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI VQIVRRIHE AAPDKDTPVN LYCRSGRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHHLNAVNI					
m768	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHHLNAVNI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VQIVRRIEAPDKDTPVNLVCRSGRAEAALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VQIVRRIEAPDKDTPVNLVCRSGRAEAALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCGC AAAACCCGT ATCCGCGCC CAAACCGCGC
 101 AACATTGAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCATTGCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCGCGCG
 201 CATACAGGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
 51 GHLHNAVNI VQIVRRIHE AAPDKDTPVN LYCRSGRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHHLNAVNI					
m768	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHHLNAVNI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VQIVRRIEAPDKDTPVNLVCRSGRAEAALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VQIVRRIEAPDKDTPVNLVCRSGRAEAALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

```

g769.seq
1  TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATGCG
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTCCCAT ATTCCGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GGCGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 AGAAAAAATG GGTCCGTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGCG AGGGTTTATC CGGGGAATAA GAAATTC AAC GATATGACGG
851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGCGCTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 GCCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCCGACA ATACCCATTG GCAAATTTCC AATTCGCTGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA
1151 ACCCGCGCGA CCGTGGCGAC AATTTC AAC GTTACGGCCT GCGCTTTGCC
1201 TGGGGGACAG AATGGGCGG CAGCGGCTGT TCTTCGCTGT TCCGCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACC CGTCTTCAGC AGTTTAAAG
1301 GGGAAAGCGC CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGGCATTGC ATTTCAAAG CATCACGCC CGCCTGACGC TGTCGCACCG
1401 CGAACCGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGCGCT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

```

g769.pep
1  LIMVIFYFYF CGKTFMPARN RWMLLP LLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 NIAGIRVILP IYLOQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
201 LRERDAWKVN GGFVSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRKKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYLGRFA
401 WQGWGSGSL SSLFRLGVAK RHYEKPGEFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAVFEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

```

m769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGGAACCG GATTGAGAA CCGCTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGAGGT
201 GCGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGC CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGAATTGAT TGCCGCCCAA
451 CCCGACGCGC CGGCCGTCCG TATGCGTTTG CCGGCAGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAGCCCG CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG AGGCGCAGCT
801 GTCCGGCAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAAAG TGCCGGGCTG
901 CAGTGTGTTT CCGAACGCGC CACCTACGGC AACGACGCTT ATCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTGCG GCCTCGGCGC

```


1251

```

1251 GCGCAACCGG CATTATGAAA AACCCGGCTT TTCAGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTG TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

```

1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAEETPREP DLRSRPEFRL
51 HEAEVKPIDR EKVPGQVREK GKVLIQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQDFRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NOAPKQQYQ KWFPPKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGDLFYR ERNPADRGDN FNRYGLRFAW
401 QEWGSGSCLS SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

```

          10      20      30      40      50      59
g769.pep  LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAEETPCEPDLSRPEFRLHEAEVKPI
          |||||
m769      LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAEETPREPDLSRPEFRLHEAEVKPI
          10      20      30      40      50

          60      70      80      90     100     110     119
g769.pep  DREKVPQVREKGVQVLDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
          |||||
m769      DREKVPQVREKGVQVLDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
          60      70      80      90     100     110

          120     130     140     150     160     170     179
g769.pep  KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAAADQFD
          |||||
m769      KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFD
          120     130     140     150     160     170

          180     190     200     210     220     230     239
g769.pep  RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYGNWTFPKQV
          |||||
m769      RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYKWTFFPKQV
          180     190     200     210     220     230

          240     250     260     270     280     290     299
g769.pep  DGTAVNYRFGAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
          |||||
m769      DGTAVNYRLGAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
          240     250     260     270     280     290

          300     310     320     330     340     350     359
g769.pep  GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNTHLQI
          |||||
m769      GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRLKNTRRARSNTHLQI
          300     310     320     330     340     350

          360     370     380     390     400     410     419
g769.pep  SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGVA
          |||||
m769      SNSLVFYRNARQYWMGGDLFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGAA
          360     370     380     390     400     410

          420     430     440     450     460     470     479
g769.pep  KRHYEKPGFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
          |||||

```

1252

```
m769      KRHYEKPFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

g769.pep   480      490
          KNRAVFVEFNKTFX
          |||||
m769      KNRAVFVEFNKTFX
          490
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```
a769.seq
1  TTGATAATGG TTATTTTSTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCGGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 CGGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCCGGT TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGATG TGTCGCCCAA
451 CCCGACGCGC CGCCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCT AGCTGTACCG CAAGGCATTG
601 CCCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAACGCGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GCGCGAAGA TGCCGGGCTG
901 CCGATGTGTC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGTTGT TTTACCGGAA
1101 TGCGGCCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCGTTCG CTTTGCTTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GGCGAAACGG CATTATGAAA AACCCGGCTT TTTACGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA
```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```
a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKRQYQ KWTFFKQVDG TAVNYRLGAE
251 KRWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAKR HYEKPGFFSG FKGERRRDKL LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```
          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90     100     110     120
a769.pep  EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
```

1253

m769						
	EKVP	QGVREK	GKVLQIDGET	LLKNPEL	LSRAMYS	AVVSNNIAGIRVILPIYLQQAQDKM
	70	80	90	100	110	120
a769.pep	130	140	150	160	170	180
	LALYAQ	GILAQADGRV	KEAISHYREL	IVAQPDAPAV	RMRLAAALFEN	RQNEAAADQFDRL
m769	130	140	150	160	170	180
	LALYAQ	GILAQADGRV	KEAISHYREL	IAAQPDAPAV	RMRLAAALFEN	RQNEAAADQFDRL
a769.pep	190	200	210	220	230	240
	KAENLP	PQLMEQVELYR	KALRERDAW	KVNGGFSVTRE	HNINQAPKROQ	YGKWTFFKQVDG
m769	190	200	210	220	230	240
	KAENLP	PQLMEQVELYR	KALRERDAW	KVNGGFSVTRE	HNINQAPKROQ	YGKWTFFKQVDG
a769.pep	250	260	270	280	290	300
	TAVNYRL	GAEEKWSLKN	GWYTTAGGDV	SGRVYPGNKK	FNDMTAGVSGG	IGFADRRKDAGL
m769	250	260	270	280	290	300
	TAVNYRL	GAEEKWSLKN	GWYTTAGGDV	SGRVYPGNKK	FNDMTAGVSGG	IGFADRRKDAGL
a769.pep	310	320	330	340	350	360
	AVFHERR	TYGNDAYS	YTNGARLYF	NRWQTPKWQ	TLSSAEWGRL	KNTRRARS
m769	310	320	330	340	350	360
	AVFHERR	TYGNDAYS	YTNGARLYF	NRWQTPKWQ	TLSSAEWGRL	KNTRRARS
a769.pep	370	380	390	400	410	420
	SLVFYRN	ARQYWMGGLD	FYRERNPAD	RGNDFNRYG	LRFAWGQEWG	SGLSLLRLGA
m769	370	380	390	400	410	420
	SLVFYRN	ARQYWMGGLD	FYRERNPAD	RGNDFNRYG	LRFAWGQEWG	SGLSLLRLGA
a769.pep	430	440	450	460	470	480
	HYEKP	GFFSGFKGER	RRDKELNTS	LSLWHRALH	FKGITPRLT	LSHRETRSND
m769	430	440	450	460	470	480
	HYEKP	GFFSGFKGER	RRDKELNTS	LSLWHRALH	FKGITPRLT	LSHRETRSND
a769.pep	490					
	RAFVEFN	KTFX				
m769	490					
	RAFVEFN	KTFX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGGAG GATTGACGA TCCCGACGTT
151 CAAGGGGTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCTATTTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCGATA AAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTGFA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

```

101	TGGGCAAAA	CGACCGTATC	GAAGTGAAG	GATTCGACGA	TCCCACGTT
151	CAAGGGGTG	CCTGTATAT	TTCGTATCGA	AAAAAAGCG	GCTTGAAGGA
201	AATGGCTAAT	TTGAAGAGG	ACGCGTCCGA	CGCATCGGTT	TCAGTCGCTT
251	AGACGGCATC	TTCGATTCT	TTTGACGAAA	CCGCGTCGCG	CAATCCGAAA
301	GAGTTTTC	AACACGGTGC	GAGCTTCGCG	TTCAGAGCC	GGCAGATTG
351	CGCTTATTAC	GACCCCAAC	GCAAAACCTT	CGCTATTGG	GTGTACAGG
401	ATAAAAATCAT	CCAAGGCTCG	CCGAAAAATT	CCTTAAGCGC	GGTTTCCTGT
451	TTCGGCGGCG	GCATACCGCA	AACCGATGGG	GTGCAAGCCG	ATACTTCCGG
501	CAACCTGCTT	CGCGGCGCCT	GCATGATTTC	CAACCCGATA	GAAAAATCTCG
551	ACAAACGCTG	A			

```

1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYIISY KKGGLKEMVN LEEDASDASV SCVQTASSI FDETAVRKPK
101 EVFKHGASFA FKSRLQIVRY DPKRRTFAYL VYSDKIIQS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

	10	20	30	40	50	60
g770.pep	MNRRLLLSAAVLPTACGSGGETDKIGRASTVFENMLGKNDRIEVEGFDDPDVQGVACYISYA					
m770	MNRRLLLSAAVLLTACGSGGETDKIGRASTVFENILGKNDRIEVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
g770.pep	70	80	90	100	110	120
	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKRGTGFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGSAFAPKSRQIVRY					
	70	80	90	100	110	120
g770.pep	130	140	150	160	170	180
	DPKRKAFAFAYLVYSDKIVQSGSPKNSLSAVSCFGSGIPQTDGVDQADTSGKLLAGACIISNPI					
m770	DPKRKRTFAFAYLVYSDKIIQSGSPKNSLSAVSCFGGGIPQTDGVDQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
g770.pep	KNPDKRX					
	:					
m770	ENLDKRX					

a770.seq

1	ATGAACAGAC	TGCTACTGCT	GTCTGCCGCC	GTCCTGCTGA	CTGCCTGCCG
51	CAGCGCGCAA	ACCGATAAAA	TCGGACGGGA	AAGTACCGTT	TTCACATAC
101	TGGGCAAAAA	CGACCGTATC	GAAGTGGAAG	GATTCGACGA	TCCCGACGTT
151	CAAGGGGGTTG	CCGTGTATAT	TTCGTATCGA	AAAAAAGCGC	GCTTGAAGGA
201	AATGGTCAAT	TTGGAAGAGG	ACGCGTCCGA	CGCATCGGTT	TCAGCGGTTA
251	AGACGGGCATC	TTCGATTCTT	ATTGACGAAA	CCGCGTGC	CCCGCGGAAA
301	GAAATTTTCA	AACACGGTGC	GAGCTTCGCG	TTCAAGAGCC	GGCAGATTGT
351	CCGTTATTAC	GACCCCAAC	CGAAAACCTT	CGCCTATTG	GTGTACACGG
401	ATAAAAATCAT	CCAAGGCTCG	CCGAAAAATT	CTTAAAGCGC	GTTTCTCTGT
451	TTCGGCGGCG	GCATACCGCA	AACCGATGGG	GTGCAAGCCG	ATACTTCGCG
501	CAACCTGCTT	CGCGGCGCCT	GCATGATTTC	CAACCCGATA	GAAATCCCG
551	ACAAACCGCT	A			

a770.pap

```
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNNDRI EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETVAVRPK
101 EVFKHGASFA FKSQRIVRYY DPKRKTFAYL VYSDKIIQGS PKNLSAVSC
```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATG GATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51  GGTGCTGACG ATGCTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCGAA AACATCCGCA GCCGCTCCA ACAAAAGCATT
151 GCCCATACCC ACCGAAAAT CTGTTTGAT GCGGATATAC GCGCAGGCT
201 TCTGCCCGCG CCGACCGTCA TCCTGAAAAA CTTGACCATT ACCGAACCCG
251 ACGCGCGCGG GGTGCGCGTT TCCGTCAAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCGGATACAG GTTGAAAAAT GGGTGGTTTC
351 GGTGCGGAT CTGCGCTGA CGCGCGACAG AACCGGCGCT TGGAAATCC
401 AAGACCTGTT CGACGGCGCG AAACACTCCG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGCAAC AGCTTATCCT
501 GAAGGAAATC AGCCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCAGT
551 TTGAAAGTTC GGGCATACTG GTTTGGAGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATCACCATT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCGCAAATC CCCGCACTGG CACTCAAAAA CAACAGCATC AAAACCGGCA
851 CGGTCAACGG CACGTTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GTTCAAAAC ACCGCGCCTT CAAACCAATT
1001 TCTCCCTCGG CTCGCCGTTG GTTTGGAGTC GGGACAACGG GCTGGACGCC
1051 CCGCGCCTGC ACATATCGAC CCTTCAGGAT ACCGTCGACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCATA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA ACCCGTTGCC
1201 GCAAAATTC AATATACGG GGAAGGCGCA CCGCACCTGG AAGCCGCGCG
1251 CGCGCTGCAA AAATTAACCC TCGCCCCCTA TCTTGACGAA TTTCCGGCAAC
1301 AAAACGGCAA AATATTCCCC GACATCCTCG GCAGGCTGTC CGGCAACGTC
1351 GAGGCACACC TCAAAATCGG CAGCATCCAA CTCCCAGGCT TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGACCATATC GCGCTCAGCC
1451 GTTTCAGATC AGGGCTTTAC GCGCGCCATA CCGAAGCGCG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA TCGGTCATC GACCTGACCG CAAGCGGCGA AAACCGCAAA
1651 CAGCTTATCC GCTCGCTGCA AGGCAGCCTG TCGCTGAATA TTTCCAACGG
1701 AGCGTGGCAC GGCATCGATA TGGACAGCAT TTTAAAAAAC GGCCTTTCCG

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1256

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1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGCGAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAUVGLH ASVYRTFTPE NIRSRLQOSI
51 AHTRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGES
101 WKNLWSDRIQ VERKVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNIS KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGLSLI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAAAQ KLNLAPLYDE FRQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDH IALSRFKSGLY GHTEGGIS I
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAASGENRK
551 QLIRSLQGS LSLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKEP
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGTGACG ATACTGCTTT TGCGCGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCGTGAA AACATCCGCA GCCGCTTACA ACAAAGCATT
151 GCACACACAC ACCGGAATAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CTGTGCCCCG CCGACCGTCA TCCTGAAAAA CCGTACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCAGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCCTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCCGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAAAT CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTACC GCCGGCGGGC AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCAGACAAAG CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGG
1051 CGCGCGCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGGGGCAAC
1301 AAAACGGCAA AATATTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAATATCGG AAAAGTCCAA CTTCGCCGCC TGCAACTGGA
1401 CGATATGGA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAAATG CAAGCAACAT
1551 CCAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGCGGGCGA AACCAGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAACTGC CGACAATGCC GCACCCAGCA CACCTTCCA CCGATTACG
1801 CTAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAAT GTCTGAAGAT GTCCTTATCC GCAACGCGGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGCGCG CATCAATTCT CGCAAGAGA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAGAAC CGTA

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— 12 —

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSLQQSIAHTRHKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSLQQSIAHTRHKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSGAD					
m771	ADIQRLLPRPTVILKNLTITEPGDQTAHSVQETKIGLSWKNLWSDQIQIEKWVVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQOQLILKEISLNLQSPDSS					
m771	LALTRDGKGVNNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQQFESSGILVWRKLSVPWKSRLGLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNISIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLDAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQNNWNAELNGTDFDRQPVAAKFYRTREGAPHLEAAAAAQ					
m771	TVNRLPQPRFISRLDGSLSVPNLQNNWNAELNGTDFDRQTVAAKFYRTHEADAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLAPYLDDEFRRQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDHI					
m771	KLNLTPYLDDEVRRQNGKIFPDILAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGHI					

1258

	430	440	450	460	470	480
g771.pep	490	500	510	520	530	540
	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	490	500	510	520	530	540
	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
g771.pep	550	560	570	580	590	
	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	550	560	570	580	590	600
	DLTAGGETRKEIRSLQGSLSLNISNGAWHGIDMDNILKNISGKTADNAAPSTPFHRFT					
g771.pep	600	610	620	630	640	650
	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	600	610	620	630	640	650
	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
g771.pep	660	670	680	690	700	
	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	660	670	680	690	700	
	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAAGCATT
151 GCCCATACGC  ACCGGAATAA  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201 TCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCATT  ACCGAACCCG
251 GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGGCGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAAATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTGCG  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACACCCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCCGCGCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAAACT  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATCC  GCCGGCGGCG  AATATGCCCA  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCCGCA  AACCCTTGCC
1201 GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCT  GACACCTTCG  CCAAGCTGTC  CGGCGACATC
1351 GAGGCGCACC  TGAATATCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCGGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAAGTC  AGGGCTTTAC  GGCAGCCATA  CCGAAGGCGG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCTCG  CAACAGAATG  CAAGCAACAT
1551 CCAATTCCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGGCA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAAACG
1701 TGCATGGCAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGCG  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTACAG
1801 CTCAACAGCG  AAATTTCAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCGET  ACGGTGGACA  AACCCTCCAT
2001 TACCGTCCAT  TACGCGAGGC  TGACCGGCGG  CATCAATTCG  CGCAAAGAGA
2051 AACAGAAAT  CCTCGAAGAC  ACCCTGCTGG  AACAATGGCA  GTGGCTCAA
2101 CCTAAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

a771.pep

```

1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
51 ANTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLTPYLDV VRQONGKIFP DTLAKLSGDI
451 EAHKIGIKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGGSI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLEQWQWLK
701 PKEP*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPEINIRSRLQQSIANTHRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSIANTHRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKWVSSAE
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNQSPDSS
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHFEASTSLDGHGITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTALARNNSIKIETVNGAFTAGGEYAQWDG
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALARNNSIKIETVNGAFTAGGEYARWDG
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
a771.pep	TVNRLPQPRFISRLDGSLSVFNQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSVFNQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
a771.pep	KNLTPYLDVVRQONGKIFPDTLAKLSGDI EAHKIGKVLPGQLDDMETYLHADKGHI
m771	KNLTPYLDVVRQONGKIFPDTLAKLSGDI EAHKIGKVLPGQLDDMETYLHADKGHI

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTCCGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGTTTTCGCG	GCGTTGGCGG
101	AAGGCAGATT	TCACCAAGTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACGCGGAA	TCGATTTTCG
201	GCGCGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGCGGACATC	GTCCGCCACC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTTG	AGATGCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTGCAACACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTC	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGGGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTC	CCTCTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGGCGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNQQ	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGCRQT
201	RADFNHDIIR	LRAHGVNDIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLVYS	SCVLEHKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTCCGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGTTTTCGCG	GCGTTGGTGG
101	AAGGCAGATT	TCACCAAGTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTTCG
201	GCGCAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTGCAACACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTC	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGGGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

m772.pap

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNH	AH				
m772	MFQAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	70	80	90	100	110	120
	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNH	ALDHFFLQHKVHIGDI				
m772	II III : : : : : : : : :					
	DGGIHFRRRVERFGYVNVQHFHIEKILQHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	130	140	150	160	170	180
	VRHLRQFEQKRRGDVIRQVADDFLFXDAVEIKLQHVAFVNHQFIRKRRQFQTAYDVAVD					
m772	: : : : : : : : : :					
	VRHLRQLEQKRCGNVVREVADDFLFCADAVEIKLQYIAFVNHQFIRKRRQFQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	190	200	210	220	230	240
	FDNVQAVQLFRQRFNGRCRQTRADFNHDIIRLRAHGVNDNIADNPRVLQKILPETLAGFVFF					
m772	: : : : : : : : : :					
	FDNVQAVQLFRQRFNGRRQTRADFNHDIIRLRAHGVNDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	250	260	270	280	290	299
	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTHRAVLVYSSCVLEHKVCVYSIRLSALX					
m772	: : : : : : : : : :					
	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVYSSCVLKHKVCVYSIRLSALX					
	250	260	270	280	290	

a772.seq

1	ATGTTCTGGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTCGAAG	CTCTTTTCGA	TGTTTGCGTA	TGTTTTCGGC	CGGTTGGTGG
101	AAGCGCAGAT	TACAGAGATT	GGCGAAATGC	TGCAATCGCT	CCGCCCTTGC
151	GATACGGTGT	TTCACCGGAA	TCATGCGGAC	GACGGCGGAA	TCCACTTTGC
201	CGCGGGGGTC	GAACGATTGC	GGCGGCACGT	CAATCAGCAT	TTCATATFCG
251	AAGAAATATT	GACGATCAC	GCCCAACCGT	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGATCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	CGACAGATCG	GTCGCCCAAC	TCCGCCAGCT	TGAACAAAGT	CGCGGCTGAA
401	ATGTTGTAGG	CGAGGTTGCC	GACGATTTTC	TTTTTCCGCT	CGATGCCGTT
451	GAATCAACAT	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGCTCAT	TTGCACAACG
551	TGCAGGCGGT	TGACGTTTTT	GCCTAAAGTG	TCGGTAATCG	CGCGCAAAAC
601	CGGACCGGAT	TCAATACCGA	CATCATCCGC	CTGCGGGGCG	ACGGCGTTGA
651	CAATATCGCT	GATAATCCCG	GTGTCTCGTA	AAAAATTCGT	TGAAACCCCG
701	TTGCGGGCCT	TGTGTTCTTT	CATCGTGTTT	CCCTTTCCGT	CGCAACCCCG
751	CCCTTTAGGG	CGGTAGAAAT	AGACTCTATT	TGGGAGGGGC	GTAACCTCCT
801	CCAAATCAGG	ACGGCACATA	GGGCGGTGCT	TTATGTCTGC	TCCTGTGTGT
851	TGAAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCCGG	ATTGTAA

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLOIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIHFRRGV ERFGHRVNOH FHIEEILQHH AQAQVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRVAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772 95.6% identity in 298 aa overlap

a772.pep      10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
m772          10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD

a772.pep      70      80      90      100     110     120
DGRIHFRRGVERFGRHVNOHFHIEEILQHHAAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI
m772          70      80      90      100     110     120
DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI

a772.pep     130     140     150     160     170     180
VRHLRQLEQKRRGNVVGQVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
m772         130     140     150     160     170     180
VRHLRQLEQKRCGNVVGQVADDFLACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD

a772.pep     190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQRTDFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
m772         190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQRTDFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF

a772.pep     250     260     270     280     290     299
HRVSFSVETPPFRVAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
m772         250     260     270     280     290
HRVSFSVETPPFRVAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTGTGCGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAATCTAG
251 CCGTATGGGG ATTGGAACG CTGATTACGC GCAAAATGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAATT TAAAACATTT GATTATTTT ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSROL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLSLTPK TADVQRNLS QSEVGKWKWK GIEGQGMPEW DYVGRGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYKSKS
251 NITVKITEIE *
```

a773.seq not found yet

-- a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACCTATCAA AACGGCAGGT
401 TTTCTGCCCG AGCCGCCCTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACTGT GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGCGCACTT GCGCGACGCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGCAGCCG
701 TACGCAACCG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAACCTTA AACGGCAAAAG TCAAAGCACT GGAACACGCA AAACACATT
251 CTTCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACCTATAAA AGCGGCAAGT
401 TTTCTGCCCG TGCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTCAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGCGCACTT GCGCGACGCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGCAGCCG
701 TGCGCAACCG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCSVLPVPEGSRTTEMPTOENASDGIPYPVPTLQDRLDYLEGKI					
m774	MKIKLPLFIIWLSVSASCSVSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDRLKEHYLNTEGGSASAHTVETAQN					
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDRLKEHYLNTEGGSASAHTVETAQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGGSIQSRSMYLLQSRARMGNCSVIEIGGRY					
m774	LYNQALKHYKSGKFSAAASLLKGADGGGSIQSRSMYLLQSRARMGNCSVIEIGGRY					
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTPGSPAARKRAAAVRKRKX					
m774	ANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTPGSPAARKRAAAVRKRKX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACC GC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATA C	GTCCAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCCGACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTGCG	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGCGGT	TACGCCAACC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pap

1	MKTKLPLFII	WLSVSAACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDRLK
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APFAMFKIGE
201	CQYRLQKQDI	ARATWRS LIQ	TYPGSPAARK	AAAAVRKR*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pap	MKTKLPLFIIWLSVSAACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT					
m774	MKIKLPLFIIWLSVSASCSASVSPVAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK					
	10	20	30	40	50	

1265

```

      70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDNRKLEHYLNTTEGGSASAHVETAQ
m774      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      60      70      80      90      100     110

      130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGSSIAQRSMYLLQSRARMGNCSVIEIGGR
m774      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      120     130     140     150     160     170

      190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTPGSPAARRAAAVRKRKX
m774      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATAT CTTAACGATG TCCAAGGCGA TACGACCATC AACCAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTTCG
601 CCGGTTATCG AAAAGGGGGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TCGCGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGACCTT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGACGCCC GGAATCAGC
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGACGCCC GGAATCAGC
951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIKGDLLV VEPRMCPADE DIALIELSDK RLVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATAT CTTAACGATG TCCAAGGCGA TACGACCATC AACCAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCGCTTACCA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTTCG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGACCTT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

```

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGTTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTTCGATTT GGCAGGCTAC GCGTGGGATA CCGAAACCC
1001 GTTCGTGGCG AATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790 98.2% identity in 342 aa overlap

a790.pep      10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGRGIKLVEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
|||||
m790          10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGRGIKLVEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW

a790.pep      70      80      90      100     110     120
GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
|||||
m790          70      80      90      100     110     120
GCPSCGNEQAAKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV

a790.pep     130     140     150     160     170     180
LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
|||||
m790         130     140     150     160     170     180
LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA

a790.pep     190     200     210     220     230     240
SVVAPSQYTFAVAMPDTSMSPVIEKGDLLVVEPRMRPADEIDIVLIELSDKRLVVAHLVID
|||||
m790         190     200     210     220     230     240
SVVAPSQYTFAVAMPDTSMSPVIEKGDLLVVEPRMCPAEDIALIELSDKRLVVAHLVID

a790.pep     250     260     270     280     290     300
IAGRMLIYQTRPSEALDLPESGVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
|||||
m790         250     260     270     280     290     300
IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI

a790.pep     310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
|||||
m790         310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTIT
51  TGGTTTGTIT TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GGCATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAC TGCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAATAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTTCTATACG TCGATAAAAT GGTTCGCGCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGCGCG GTTGCCTTGG
1151 ACAGCGCGCG CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGCG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCGCGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCCGA TTTCCTGCCG GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTGCG ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTGCGC CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGACAGG TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TCGGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGTACGGC CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATCCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGC CTGAAGGTGT GGTGACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1 MVNYYSAMIK KILTTCTGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYLINNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLRAQ OPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLMLDN
751 SGIAFPQSRK AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCGGT CTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GGCAGTTTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGTC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAMLGLPKAPSAYNPINVPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAMLGLPKAPSAYNPINVPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFRDGSRYGAENYIDLKSKEDVEETVSQYLSGLYTVDKMVP					
m791	RADHQKVATEALRKALRNFRDGSRYGAENYIDLKSKEDVEETVSQYLSGLYTVDKMVP					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTVKKKNVVIQLPGGRRVALDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
m791	VVLDTVKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPPLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPPLQGALGSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFSPSELPAISLMSALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSSELPAISLMSALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG					
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKGK					
m791	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSVSSNGEYYMKERMVTDPLGLMLDNSGIAFPQPSRRAKEDDEAAVENEQQRSD					
m791	MKMPEGVSVSSNGEYYMKERMVTDPLGLMLDNSGIAFPQPSRRAKEDDGAAGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTCAC ACGCAAAATC
451 AATGAGGTGT TGCTTGCTTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTGAG CCGGCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTTC ATAAGAAATG CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTCCGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAT GCATTACGAG CGGTTGTTC GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCTTAT ACGCAGGGT TTAAGGTTA TACCACGGTC
901 CCGCGCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CCGGCGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTTTGG ATGTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCCG CCGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCGCGG CCGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGT ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCGAGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGG CGCTGGTCGG CGGTTATGAT
1351 TTTCAACGCA AAACATTCA TCGTGCCGT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAT GATGCGCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGTCGCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCTATATT ATGTATAAGA
1901 TTATCGACGA TGTGTCCTG GTTGTCAGG CAAGGGGGG AGCTGCGTTG
1951 GGAAGAACCG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGTACGG CCGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CCGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CCGCGCAACC TTCCGACGG GCAAAAGAA ATGACGGGGG
2301 CCGCGCAGAA GCGGACGGC AGGCGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep
1 MVNYYSAMIK KILTTCTFLV FGFCVFGVL VAIAILVTYP KLPSLDSLOH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTKRF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLGA LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TOGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDMKMPA VVLDVTKKKN VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLRAQ QPLVAGONAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVVGGTI
701 AVPVVVDYMR FALKGKQKGG MKMEPEGVSS NGEYMKERM VTDPLGLDN
751 SGIAFPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPV LPSNTGSKQQQ
801 LDSLF*

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

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a791.pep  MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791      MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
a791.pep  SADGEVIGMYGEQRREFTKIGDFEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
|||||
m791      SADGEVIGMYGEQRREFTKIGDFEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
          70      80      90      100     110     120

          130     140     150     160     170     180
a791.pep  GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
|||||
m791      GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
          130     140     150     160     170     180

          190     200     210     220     230     240
a791.pep  RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE
|||||
m791      RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE
          190     200     210     220     230     240

          250     260     270     280     290     300
a791.pep  EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
|||||
m791      EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
          250     260     270     280     290     300

          310     320     330     340     350     360
a791.pep  RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
|||||
m791      RADHQKVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
          310     320     330     340     350     360

          370     380     390     400     410     420
a791.pep  VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
|||||
m791      VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
          370     380     390     400     410     420

          430     440     450     460     470     480
a791.pep  AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
|||||
m791      AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
          430     440     450     460     470     480

          490     500     510     520     530     540
a791.pep  KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
|||||
m791      KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
          490     500     510     520     530     540

          550     560     570     580     590     600
a791.pep  GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
|||||
m791      GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
          550     560     570     580     590     600

          610     620     630     640     650     660
a791.pep  DRDGRRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
|||||
m791      DRDGRRLAQMQPLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
          610     620     630     640     650     660

          670     680     690     700     710     720
a791.pep  TTNDNKDAWFGFNPDDVTVAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKGK
|||||
m791      TTNDNKDAWFGFNPDDVTVAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKGK
          670     680     690     700     710     720

          730     740     750     760     770     780
a791.pep  MKMPEGVSSNGEYYMKERMVTDPLGLTDNSGIAPQPSRRAKEDDGGAAEGGROAADDEV
|||||
m791      MKMPEGVSSNGEYYMKERMVTDPLGLTDNSGIAPQPSRRAKEDDGGAAEGGROAADDEV
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1268

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451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGCTGCG
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTT GGAATTCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGGCAGCA GCTACCGCGG TCGGGAACAT TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGCGCGCG CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTTCG CGGTTATGAT
1351 TTTACAGACA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTGACCTTTT AAGCCGTTTG TCTATTGCGG GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTGCGT CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTGCGC CGCCCAAAAT CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGACAGG TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGGCTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCT CTGAAGGTGT GGTACGACAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCACGCG GCAAAGAAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAACG GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

```

m791.pap
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEP LLQG ALGSLDARTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRAQM QPLVAGQNAQ QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVUTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYYMKERM VTDPLTLN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSL*

g791/m791 97.3% identity in 805 aa overlap

          10      20      30      40      50      60
g791.pap  MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
g791.pap  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          70      80      90      100     110     120

```

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```
1 ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCA tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGAAGAGGCG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAATCAATC GAATGGCACT ACGGCgtTTT
501 CGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgy tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgy ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaagcg aaacggactg
701 attgttccag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa
```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```
1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAA KLTVLVPAPF
201 YYSDHKSKR LRNKTNIIVL RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```
1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTGT AACTGTATTT AAATCAATC GAATGGCACT ACGGCGTTTT
501 CGCGCGGAA GCGCGTCCC GGTATTTTA TCAAAATACC GCCGCCAAGC
551 TGACCAACA GCAGGCGGCA AAATGACGG CCGCGTCCC CGCCCCGCTC
601 TACTACGCC ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAA CGCATGGGT CGGCAGAGT GCCTGAAAGC GACACGGACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```
1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAA KLTARVPAPL
201 YYADHFKSKR LRNKTNIIVL RMGSAELPES DTD*
```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

m792	WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK	70	80	90	100	110	120
		130	140	150	160	170	180
g792.pep	NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEASRYFYKKP						
m792	NLFLNESRSYIRKGEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEASRYFYQIP	130	140	150	160	170	180
		190	200	210	220	230	240
g792.pep	AADLTQQAAKLTVLPAPFYYSDDHPKSKRLRNKTNIVLARMGSANYPKAKRTDCSRYGN						
m792	AAKLTQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLKRMGSAELPESDIDX	190	200	210	220	230	
		250					
g792.pep	AAXTGVRTAYVFDLX						

```

a792.seq
1      ATGTTCCGCA  TCATCAAATG  GCTGATTGCC  CTGCCCGTCG  GCATCTTTAT
51     CTTTTTCAAT  GCGTATGTGT  ACGGCAACAT  CATTACCTAC  CGCGCCGTCG
101    CGCCCCATCG  GACTGCCTTT  ATGTCGATGC  GGATGAAGCA  GTTTGAACAG
151    GAAGGTCGCG  ATGTCGCATC  GGATTACCCG  TGGATGCCCT  ACAAACGCAT
201    TTCCACCAAC  CTGAAAAAAG  CCTCGATTGC  TTCCGAAGAT  CGCCGTTTCG
251    CGGGGACCGG  CGGCTTCGAT  TGGGGCGGCA  TTCAAAAAGC  CATCAGGGCG
301    AACCGGAACA  CGGGCAAAAT  GAGGGCGGGC  GGCTGCAGCA  TCAGCCAGCA
351    GCTTGCCAAA  AACCTGTTTT  TAAACGAAAG  CCGCAGCTAT  ATCCGCAARA
401    GCGAAGAAGC  GGGCATTTAC  CGGATGATGG  AAGCCGTTAC  CGCAACAAAT
451    AGGATTTTTG  AACTGTATTT  AAATCAATC  GAATGGCATC  ACGCGGTTTC
501    CGGCCGCGAA  GCGCGCTCCC  GGTATTTTTA  TCAAATAGTC  CGCGCCAAAG
551    TGACCAACA  CAGGCGGGCA  AAATGACGG  CGCGCGTCCC  CGCCCGCGTC
601    TACTAGCCG  ACATCCGGAA  GAGCAAAACG  CTCGCAACA  GAACCAATAT
651    CGTGCTCAGA  CGCATGGGTT  CGGCAGAGTT  GCCTGAAAGC  GACACGGACT
701

```

```
a792.pap
1  MFRIIKWLIA LPVGIFIFFN AYYVGNIIYT RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGDFD WGGIQNAIRL
101 NRNSGKVKAG GSTISQQLAK NLFNLNRSRY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI ENHWYGVFGE AASRYFFQIP AAKLTQQQAA KLTRVPAFL
201 YYADHEPKSR LNRKNTINVLRL RMGSAELPES DTD*
```

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a792.pep	WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK					
m792	WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRNRNSGKVKAGGSTISQQLAK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a792.pep	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRI FELYLNSIEWHYGVFGAEAAASRYFYQIP					
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRI FELYLNSIEWHYGVFGAEAAASRYFYQIP					
	130	140	150	160	170	180
	190	200	210	220	230	
a792.pep	AAKLTQQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSALPESDIDX					
m792	AAKLTQQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSALPESDIDX					
	190	200	210	220	230	

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1274

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1  ATGTTGATTA  AAAGCGAATA  TAAGCCCCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATTAGCTTC  GTCCTGATGG
101 CAATGGCCGT  CTTGTTTGCC  TGTCTGATTG  CCCGCGGCT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GGCACAAACC  GGATTGTGCG
201 GACTCAAACA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGCGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCCTAAA
301 GATATGAAGG  AAATGCCGTC  TGCCGCCCAA  TTGGAACGCC  TGTCAGAGCT
351 TGTGATGTG  CCGGTCGATG  TTTTGAGGAA  CAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  TTGGATCAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAG  AATTAAACCG
501 CCATTACCCG  ATGGGCAACC  TGTTGCACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 TATGGCGAAG  ACGGCGCGGA  AGTTGTTTGT  CGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGACTCCC  CGCGCAATA  AGCACCGCAA  AACGGCAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGACCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCTGGTTCG  GCAATCAAAC  CGTTCGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCGGA  CCGTCTCCCG  TGCGCGATGA  TACCCATGTT
1051 TACCCCTCTT  TGGATGTGCG  CGGCATTATG  CAGAAATCGT  CCAACGTCGG
1101 CACAAGCAAA  CTGCTGCGC  GTTTCGGCGC  CGAAGAAATG  TATGACTTCT
1151 ATCATGAATT  GGGCATCGGT  GTGCGTATGC  ACTCGGGCTT  TCCGGGGGAA
1201 ACTGCAGGTT  TGTGAGAAA  TTGGCGCAGG  TGCGCGCCCA  TCGAACAGGC
1251 GACGATGTCT  TTCGTTACG  GTCTGCAATT  GAGCCTGCTG  CAATTGGCGC
1301 GCGCCTATAC  CGCACTGACG  CACGACGGCG  TTTTGCTGCC  GCTCAGCTTT
1351 GAGAAGCAGG  CGGTGCGCC  GCAAGGCAAA  CGCATATTCA  AAGAATCGAC
1401 CGCGCGCGAG  GTACGCAATC  TGATGGTTTC  CGTAACCGAG  CCGGGCGGCA
1451 CCGGTACGGC  GGGTGGGTG  GACGGTTTCG  ATGTCGGCGC  TAAACCGGCG
1501 ACGGCGCGCA  AGTTCGTCAA  CGGGCGTTAT  GCCGACAACA  AACACGTCGC
1551 TACCTTTATC  GGTTTTGCCC  CCGCCAAAA  CCCCCGTGTG  ATTGTGGCGG
1601 TAACCATCGA  CGAACCGACT  GCCACGGCT  ATTACGGCGG  CGTAGTGGCA
1651 GGGCCGCCCT  TCAAAAAAT  TATGGGCGGC  AGCCTGAACA  TCTTGGGCAT
1701 TTCCCGGACC  AAGCCACTGA  CCGCCGCGAG  CGTCAAAACA  CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR  MLPKEEQVKK  PMTSNGRISF  VLMAMAVLFA  CLIARGLYLQ
51  TVTYNFKLEQ  GDNRIVRTQA  LPATRGTVSD  RRGAVLALSA  PTESLFAVPK
101 DMKEMPSAAQ  LERLSELVDV  PVDVLRNKLE  QKGKSFIIWK  RQLDPKVAEE
151 VKALGLELNFV  FEKELKRHPY  MGNLFAHVIG  FTDIDGKGQE  GLELSLEDSL
201 YGEDGAEVVL  RDRQGNIVDS  LDSPRNKAPO  NGKDIIISLD  QRIQTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRP  RADSEQRNR
301 AVTDMIEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPKIG  PSPVRDDTHV
351 YPSLDVRGIM  QKSSNVGTSK  LSARFGAEEM  YDFYHELIG  VRHSGFPGE
401 TAGLLRNWRR  WRPIEQATMS  FGYGLQLSL  QLARAYTALT  HDGVLLPLSF
451 EKQAVAPQGG  RIFKESTARE  VRNLMVSVTE  PGGTGTAGAV  DGFVDVGATG
501 TARKFVNTRY  ADNKHVATFI  GFAPAKNPRV  IVAVTIDEPT  AHGYYGVVVA
551 GPPFKKIMG  SLNILGISPT  KPLTAAAVKT  PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCCGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GGCACAAACC  GGATTGTGCG
201 GACTCAAACA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGTGC  CCGACGGAGT  CCCTGTTTGC  CGTGCCCTAAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCAGAGCT
351 TGTGATGTG  CCGGTTGATG  TTTTGAGGAA  CAAGCTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAG  AATTAAACCG
501 CCATTACCCG  ATGGGCAACC  TGTTGCACA  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTCGAAC  TTTGCTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTGT  CGGGACCGGC  AGGGCAATAT
651 TGTGGACAGC  TTGACTCCC  CGCGCAATA  AGCCCGGAAA  AACGGCAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCAATA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGGCCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCCGGTTTC  GCAATCAAAC  CGTTTGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA

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1275

```
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGC GCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCCG
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGCGCACCG
1451 GTACGGCGGG TCGGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 CCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMIAVLFA GLIARGLYLQ
51  TVTYNFIKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFXHELGIGV RMHSGFPGET
401 AGLLRNRRWR RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYVGGVVAG
551 PPFKKINGGS LNILGISPTK PLTAAAVKTP S*
```

g793/m793 98.5% identity in 582 aa overlap

g793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
g793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
g793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
g793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
g793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
g793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	360
g793.pep	370	380	390	400	410	420
m793	370	380	390	400	410	420

1276

```
          430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALTHDGVLLPLSFQKQAVAPQGRIFKESTAREVRNLMVSVTE
          |||
m793      FGYGLQLSLLQLARAYTALTHDGVLLPVSFQKQAVAPQGRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||
m793      PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          |||
m793      AHGYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```
a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCCGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGTATTGTCG
201 GACTCAAACG TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCAGGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAA GCGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAG AATTAACCG
501 CCATTACCCG ATGGGCAACC TGTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CGGGACCGGC AGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGCTAACCG ATATGATCGA ACCCGGTTCC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCGGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```
a793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNLFKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYF MGNLFAHVIG FTDIDKGQGE GLELSLEDSL
201 HGEDGAIEVL RDRQGNIVDS LDSPRNKAPK NGKDIIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFFYHELIGIV RMHSGFPGET
401 AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*
```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLESLSDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLESLSDSLHGEDGAEEVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMDFYHELIGVGRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMDFYHELIGVGRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALHDGVLLPVSFEKQAVAPQKRIKSTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALHDGVLLPVSFEKQAVAPQKRIKSTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTTCCCACT TATCCGGCTT
101 TGCCATTATA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCCG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GTCGTTACC GCGTTGCCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTGTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCGTCCG CTTGCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACCGG CTTATTTTCA
1251 CCGGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GCGTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAAGGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1 VRENHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLT GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVGSF DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKML RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGSD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRK
451 TGTLLNNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDAKLMC KERRA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1 GTGCGTCTCA ATCATTTTCA ATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGGGCC GCGGCCACAG CGTTCCTACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCAGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CTTCAAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTTGGCGGG CAGCGGCGAC
451 CCCGTTTTC ATCAGGAAAA CCTGCTTGAT GCTCAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCTATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCTGCTC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGC CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAACCGG CTTATTTTCA
1251 CCGGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GCGTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAAGGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSVDPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQKQLREQGI LNTIGHLM LD HSLWGEVGS DFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLV L ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

```

-- g794 --
      10      20      30      40      50      60
g794.pep VRENHFIMVTIIIVISPA NKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     VRLNFHIMTAIIIVISPA NKPARRHVPTYPALPYNCFYVTDLP MNFPKTAASLLLLL
      10      20      30      40      50      60

      70      80      90     100     110     120
g794.pep ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90     100     110     120

      130     140     150     160     170     180
g794.pep NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHMLD
      130     140     150     160     170     180

      190     200     210     220     230     240
g794.pep HSLWGEVGSDFEADSGSFFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     HSLWGEVGSDFEADSGSFFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240

      250     260     270     280     290     300
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     QNNLKITASQAACPSIKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300

      310     320     330     340     350     360
g794.pep NRWLLGGGRI SDGIGIADTP EGAQTLAVAHAKPMKEILTD MNKRSDNLARSVFLKLGSD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     NHWLLGGGRI SDGIGIADTP EGAQTLAVAHAKPMKEILTD MNKRSDNLARSVFLKLGSD
      310     320     330     340     350     360

      370     380     390     400     410     420
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
      370     380     390     400     410     420

      430     440     450     460     470     480
g794.pep QDFIDTLPIAGTDGTLRNRFKQSGGLRLKGTGLNVRALAGYWLGDKPM AVVVIINSGR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     QDFIDTLPIAGTDGTLRNRFKQSGGLRLKGTGLNVRALAGYWLGDKPM AVVVIINSGR
      430     440     450     460     470     480

      490     500     510
g794.pep AVSLLPDLDNFVAKNIISGGDGWLDKLMCKERRAX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     AVSLLPDLDNFVANNIISGGDGWLDKLMCKERRAX
      490     500     510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

```

1   GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCGCATTC CGCAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGCGGG CAGCGGCGAC
451 CCCGTTTTC ATCAGGAAAA CCGTGTGTC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGATCTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCGA GAGCTGTTT GGCAAGCCTG
851 TCGGTGTCCG GATGTTGCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAACT CCGCGCGGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCA GCGCTGCGG TCCGCGCTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTG GAAAACGGT CAGGTCTGTC CAGAAAAGAA
1201 ACGGTAAACG CGAATATGAT GCGGCAATG TTGAAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTCA TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GCGTGGCGCA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGGC
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51 KTAASLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NFASTMKLV AFAPKTFGS NYRWATEFKS NGTVNDGTL GNLYWAGSGD
151 PVFNQENLLA VQRQLREQI RNITGHLMLD HSLWGEVGS DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLV ENSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRK QSGGLLRK
451 TGTLLNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

a794.pep	10	20	30	40	50	60
m794	10	20	30	40	50	60
a794.pep	70	80	90	100	110	120
m794	70	80	90	100	110	120
a794.pep	130	140	150	160	170	180
m794	130	140	150	160	170	180
a794.pep	190	200	210	220	230	240
m794	190	200	210	220	230	240
a794.pep	250	260	270	280	290	300
m794	250	260	270	280	290	300
a794.pep	310	320	330	340	350	360
m794	310	320	330	340	350	360

g900.seq

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

g900.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

1 ATGCCGCTGTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT
51 TCAACGGGCG GATGcCGACC GCATCg.TA CTTTGTCcAA TAATTcCGGT
101 GCTTCcTTTAC GCGCtTTTCG CGCGCCTGCC TGcAAAATCT CTTcGATTtG

1282

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCCGCCCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GCGTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TGGGTTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXVFQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRQKFFGFT PRQAVGKHFR KFHRRRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQFDF VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQLT
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

```

              10      20      30      40      50
m900.pep      MPSETRQAEVRTASGSFQRADADRIXVFQXFACFFTRFRRAACLQNLFDLRRVGGQ
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900          MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRAACLQNLFDLRRIRGQ
              10      20      30      40      50      60

              60      70      80      90      100     110
m900.pep      LVVAFARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRRGEFGVDFKQWAFVGLFRL
              ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| : |||||
g900          CVVAFQAQFCQFGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEFGFIDFKQRAVGLFRL
              70      80      90      100     110     120

              120     130     140     150     160     170
m900.pep      ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFHGFASVQTDQFDFVFIDFHFGQGEFPEA
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900          ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVGFHGFASVQTDQFDFVDFVDFHFGQGEFLET
              130     140     150     160     170     180

              180     190     200     210     220     230
m900.pep      VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL
              ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900          VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTIGVFLPVFRIGL
              190     200     210     220     230     240

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      240      250      260      270      280      290
m900.pep HGGFVGMGAHVHQTLSGDAQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:||||:|||||||:||||:|||||
g900      NGGFVGVGAHVHQTLLGGDAQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFFAHKNVL
          | |||||:|||||
g900      LLLVAFDDAVVIGEEEEFGFIVLRRADGGADGADVVAQMRGAGGGYAGQNSFFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep AAMPSEEREKDVPIIPDLPTSSRQQTFFPYX
          :|:|||||:|||||
g900      TAAMPSEEREKDAPIIPDLPHPTSSRQQTFFPYX
          370      380      390

```

```

a900.seq (partial)
1 GAGGTCGCGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51 CACGTACTTT GCCCAATAAT TCGCGTGCTT CTTTACGCGC TTTTTCGCGC
101 CCTCGCTGCA AAATCTCTTC GATTTCGCAA GGTCGCGCGG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTCCG CGAGTTCGCG GTTGATTTCG CGCGCCAAAA
201 GTTTTTTTTG CTGCGCCCCA GCCAAGCCGT CGCAAGCAT TTTCTGTAAT
251 TCTGCGGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATT CAAACAGAGG
301 GCTTTCGTCG GGCTTCTTCG CTGCGCCGG CTCTTTCATA TTGGTGATGA
351 TTTTGTGAC CGATTTTGG GTTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTGTCCGT AGGTATTGGA CATTTGCGT CGGTCCAAC CAACCAAGAG
451 TTCGACGTTT TCGTCGATT TCACTTCGGG CAGTGTGAAG AGTTCCCGGA
501 AGCGGTGGTT GAAGCGGCCG CCAATATCGT GTGCCATTTC AACGTTGTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCAGTCATG AGGATAGGTT AGCTGTACAA ACCATTTC CCGCCGAAAT
651 CGGGTCTTTC TGCCCGTTT TCCGCATTG CTGACACGGC GGCTTTGTAG
701 GCGTGGGCGT GGTTTCACAA ACCCTTGGCG CGTATGACAG TCGAAGTCCA
751 GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGACG GCAGCCAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGAA TCATCTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAATC
901 GGCAGGAAG AGGAAGGATT CGGTATCAGG GTTTTGCGCC GCGCGGACGG
951 CGGGGCGGAT AGCACCACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTAATGCCG TCAGAACTCG TTTTGTGCTC ATAAAAATGT CCTTGGCGCA
1051 TCAATGCCGT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTTGCC
1101 ACCTACATCC AGCCGACAA AGACTTTTCC ATATTAA

```

a900.pap (partial)

1	EVRTALGLFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV
51	VAFARFGEFG	VDFRRQKDFC	LAPSQAVGKH	FRKFCFRFR	GESFVDFQOR
101	FAFVGLRLAR	LFHIGGDFVD	RFLGFVVVF	KRNGVAVGFG	HFAFVQHTNE
151	FDFVDFHFHG	QCEEFEPAVV	EAGNIACHF	NVLDLVATDW	NFMGIEHQNV
201	GSHERDRAVQ	THFHA <u>EIGV</u>	LPVFRICLHG	GFVGVGAVHQ	TLGGDAGQNP
251	VQHFHFNGVA	LVTEGGALGV	ESACKPSGND	GLGGLVNHLR	LVAFDDTVVI
301	GEHEEGFGIR	VLRRDGGAD	SDTVAQMRD	AGGGYAGQNS	FFAHKNVLAA
351	SMPSEREKDA	PIIPDLPTTS	SRQVTFPY*		

```
m900.pép      MPSETRQAEVRTASGSFQRADADRIXYFVOXFACFFTRFRRAQLQNLFDLRRVGGLVVVA  
              ||||| :|||||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~:  
a900          EVRTALGLFQRADTDRIITYFAQXFCFFTRFLRAQLQNLFDLRRVGGLVVVA  
               |    |         |        |           |             |  
              70       80       90       100      110      120
```

1284

```

m900.pep  FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
          |||||:| ||||| |||||:|||||
a900      FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRRRRGESFVDFKQRAVGLLRLARLF
          60      70      80      90      100     110

          130      140      150      160      170     180
m900.pep  HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTDQEFDFIDFHFQGEFFPEAVVEA
          |||||:| ||||| |||||:|||||
a900      HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTNQEFDFVDFHFQGEFFPEAVVEA
          120     130     140     150     160     170

          190      200      210      220      230     240
m900.pep  AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
          ||::| ||:|||| | :||:||||:|:|:| ||||:| |||||:|||||
a900      AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
          180     190     200     210     220     230

          250      260      270      280      290     300
m900.pep  VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNLRLV
          ||:|||||:||||| |||||:||||| |||||:||||| |||||:|||||
a900      VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNLRLV
          240     250     260     270     280     290

          310      320      330      340      350     360
m900.pep  AFDDTVVIGEEEGFGIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          |||||:|||||:||||| |||||:||||| |||||:||||| |||||:|||||
a900      AFDDTVVIGEEEGFGIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          300     310     320     330     340     350

          370      380
m900.pep  PSEREKDVPIIPDLPTSSRQQTFFPYX
          |||||:|||||
a900      PSEREKDAPIIPDLPTSSRQQTFFPYX
          360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTCGATGTC CAATTGGGCC GTTGCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTakGyAG TGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGCGGGT
151 GCGATGGTAT ATGTTTCCCT GACGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
401 CGCACAAATT CCCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGTATCCG GCTTGGCCGA GCCGTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGCGTGA TAGCCGTTG GATGGTGTGTT TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACGTT
751 TACGGCCTGA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP

```

1285

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTTGMAVI AVSLVLFHF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq
 1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATTACGTT
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTG GTTTGGCATT TGCCGGCGGT
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
 301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
 401 CGACAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGCCGA GCCGTTGGGG
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGCTGT GATGGTGT TTTGGCGTTG
 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep
 1 MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG
 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELPAA KRYSDGHETV
 251 YGLTMGMAVI AVSLVLFHF*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
a901	MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLV NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLV NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
	RSRKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELPAA					
a901	RSRKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELPAA					
	190	200	210	220	230	240
m901.pep	250	260	270			
	KRYSDGHETV YGLTTGMAVI AVSLVLFHFX					
a901	KRYSDGHETV YGLTMGMAVI AVSLVLFHFX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTGCGCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgCggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTGGT CTCGGcgaTg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TCGGTGcgG CGcgccgTg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgTcg tgccaaccCa AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTCTcttg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcGg
801 catCCGCCAT CtggtcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTcCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCga TGGGgTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALFPPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGNAAIF GDFG DGGQVL
201 IVVPTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLPE SDVVTRRIH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTGTA TTTCACGACG
151 TgTCTgTTcG CCGTcGGGCA TTTcGTcGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTcGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GGCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTcGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCTTcGCGC GCGCGCCCT ATCATAAATG CGTCGGCGGC GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTcG CGGCGAAGTA ATGTcGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTcGGC GATGAGTTcG TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTcGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTcGCTG GTCAGCATT CGCACACCGC CCAACTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTcGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCGG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1287

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGRR
101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFPIAARPTVGFGSKPFKITGKCVVLRRIQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQQTQGRRQNTVFGIMFQIAEEPRPA				
g902	60	70	80	90	100
	ADVVPAYVFACDAHTDGLTIKRVHGADVQNGGSFAFQQTQGRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGGGFLRRSDVAVDPGRDVQTAFLGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVHLQRATGL				
g902	180	190	200	210	220
	NGKGGNAIFGDFGDDGQVLIIVVPTQTGFEGNGYARRLDHRLQNGGNQRLVHLQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHVVDKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAHIDVDDLRPESDVVTRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHRPTCAKRPTAAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCAGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

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101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTTCG
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTGTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATGTCGCGCT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAAGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 CGGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCCCAT CGGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRSA LR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNA RH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *
```

m902/a902 94.7% identity in 360 aa overlap

m902.pep	10	20	30	40	50	60
	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD					
a902	LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD					
	10	20	30	40	50	60
m902.pep	70	80	90	100	110	120
	VPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQCQTQGRRQNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDAHTGGVAVKRVHGSDDVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRSA LR					
	70	80	90	100	110	120
m902.pep	130	140	150	160	170	180
	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGNDEFTVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	190	200	210	220	230	240
	KGGDAAFGDFGDDGQVLMVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAAFGDFGDDGQVLMVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	250	260	270	280	290	300
	ADFFSGTAHVDVDKLRPKADVVTGRIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHVDVDKLRPKADVVTGRIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	310	320	330	340	350	360
	RVAGQHFAHRPTCAKISAKSAERFVGNA RH RRCDCGVVDKIAADVHNGSAFQKSTPLYIF					

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|||||
a902  RVAGQHF AHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

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m902.pep  X
          |
a902      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcg gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGaAT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCCTcaaa ccaTGCCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCC GACTGCGGAA
451 CCGGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAc GTCTGTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAaAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCTTTTC
751 GGTAaATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAaACTGTG GACGAGGGAA ACAaAAGTT ACATTGATGA
951 TGCCGAAC TGCTGACAAC GGCGTAAaAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAaAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCcCGCTA ACATCGCAAG ACAaACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTAAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAaAGCC cgaatattt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQA VSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRT KSYIDDAEL TVQRRKTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGWE WRNDLSWQFK
451 PGHQLYLGLD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFQ VGYSF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAATGT
51  CCGTTTCGAG CAACCATGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGGAATTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TCGTCGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GCGCACAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATT C AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCC CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903 .pep

```

1 MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV
51 RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNFPLYRNN
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQNKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKDTLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNVDYNGKQ
301 YQSSLAERM LWRNRLHKT S VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTMQRSM PAPEENGDI LPGTSRMKII
401 TASLDAAPF XLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYL G ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903 .pep  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |:::| |:::| |:::| |:::|
g903      MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90      100     110     120
m903 .pep  MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
          : : | : | | : : : : : : : : : : : : : : : : : : : : : :
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGT TTRILAAPQDLNSGKQLQLTMPGYLR
          40      50      60      70      80      90

```


[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACC	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTT	ATGAAAGAAA	CAGCTTTTAA
201	AAC TGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCTACC	TCAC TTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTG	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TTCGCGATGT	ATGACAGGGC	TTGGAARAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTAGCATTAT	ACCGTCCGAA	GAGGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAAACCAT	ACGGTTTCAGT

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601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCGCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGCGGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGGAT TGGATGCAGC GGCCCGGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCACTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

a903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NNKFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSSLAERM LWRNRFHKTS VGMKLWTRQT KYIIDAEIE VQRRRSAGWE
351 AELRHAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGSGT IPGTSRMKII
401 TAGLDAAAPF MLGKQFFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |||
a903      MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTARKFSFLPSVL
          10      20      30      40      50      60

          70      80      90     100     110     120
m903.pep  MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL KLRVSAGEIG
          |||
a903      MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL KLRVSAGEIG
          70      80      90     100     110     120

          130     140     150     160     170     180
m903.pep  DIRYEKRDG KSAEGSISAF NNKFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE
          |||
a903      DIRYEKRDG KSAEGSISAF NNKFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE
          130     140     150     160     170     180

          190     200     210     220     230     240
m903.pep  EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVALSFDNPLGLSDFYVSYGRGL
          |||
a903      EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVALSFDNPLGLSDFYVSYGRGL
          190     200     210     220     230     240

          250     260     270     280     290     300
m903.pep  AHKTDLT DATGTETESGSR SYSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
          :
a903      VHKTDLTDATGTETESGSR SYSVHYSPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ

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1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSGVMKLTWRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSGVMKLTWRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQOFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENGDDIPGTSRMKIITAGLDAAAPFMLGKQOFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCCGCGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCCGCGCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGAATGCA
301 CATAACCGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGCCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAAGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCTT CAAACAGCAG TTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCGgggac acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRRFAV GAGDDGDRR AADFFNPFQI CFGIGRCVV AFHADSRFAP

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1294

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51  AGHGFVNRF A GFHRI RTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRS G
251 VMQVLELDV V IGKDG IQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAF AARCF AGLVERDVVR QDQ RAGR RDF QTAFDV FHAC RVQLVDF AQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

m904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCCGTG GAGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTTCGCGCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTCTG CCAAACCTAC GCCTACTTCG TCGAACAAAT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCAGTCT TCCGCTTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTCGAGTT GGACATTGTA ATAGGCAAGG ACGCATCCA
801 GTTTTTCACG CAGTTTytCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCCG GCGCGTCTGT
901 GCCGATTTTG CCTTTGCCGC GCG.ATcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCACA AAATGGTTT TTTGCCGCCG
1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTaT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

m904.pep

```

1  MMQHNRFFSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
51  AGHGFVNRLA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAF AAXIF AGLVERDVVR QDQ RAGR RDF QTAFDV FHAC RVQLVDF AQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

```

m904.pep      10      20      30      40      50      60
               MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904          10      20      30      40      50      60
               MMQHNRFFAVGAGGDDGDRRAADFFNPFQICFGIGRCVVAFHADSRFAPAGHGFVNRF
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
               70      80      90      100     110     120

```

1295

```

m904.pep  GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       GFHRI RTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA
          70      80      90      100     110     120

          130     140     150     160     170     180
m904.pep  AAACASGYRTEFVSAFQCYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
          |||  :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
          130     140     150     160     170     180

          190     200     210     220     230     240
m904.pep  CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
          |  :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       RAGETVGRGNEGVS AVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
          190     200     210     220     230     240

          250     260     270     280     290     300
m904.pep  HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTFQFXRMQQIGGANGAACHFVFGGRADAAAGR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       HHVFRFNRSQVMQVLELDVIGKDG IQFFTFQFXRMQQIGGANGAACHFVFGGRADAAAGR
          250     260     270     280     290     300

          310     320     330     340     350     360
m904.pep  ADFAFARIFAGLVERDVVRQDQRAGRRDFQTA FDVFHACRVQLVDFAQQGFGGDDNART
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       ADFAFARCFAGLVERDVVRQDQRAGRRDFQTA FDVFHACRVQLVDFAQQGFGGDDNART
          310     320     330     340     350     360

          370     380     390     400     410     420
m904.pep  DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAAL EAHHAAGFFRQPVNDFTTTLVAPLC
          |||  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|  :|
g904       DEAIQSFVQDTARNQAQNGFFAADNQGMARIVAAL EAHDAAGFFRQPVNDFTTTLVAPLC
          370     380     390     400     410     420

          430
m904.pep  ADXYNIFSHSHITYRYX
          ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g904       ADYYNIFSHSHITYRYX
          430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

```

a904.seq
1  ATGATGCAGC ACAATCGTTT CTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATACCGGAA ATGCCGTTGA TTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTGC TCCGACTTCG TCGAACAATT CCGTCCGGAA
451 CGGGCCCCGA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGGCCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC CGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTTGCAGTT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTCACG CAGTTTTCAT GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGC GCGATGCTTC TCGGCTTGG TCGAGCGCGA

```

1296

```

951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGGTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCGC
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

```

a904.pep
1  MMQHNRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHLRG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADEFAAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

m904.pep	10	20	30	40	50	60
	MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA					
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAESGFAPTGHGFVNRLA					
	10	20	30	40	50	60
m904.pep	70	80	90	100	110	120
	GFHRIGTARQDVGFVAAGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA					
a904	GFYRIRAARQDVGFVAAGQFVADADIDGFNAVHYIEFGNTHGTGNAVDLDGAFQGGGIKPA					
	70	80	90	100	110	120
m904.pep	130	140	150	160	170	180
	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIQHLRTYARACRS					
a904	AAACASGYRTEFVSAFCQTCSDFVEQFGRERARTDARGIGFDDAQNIQHLRAYARACRS					
	130	140	150	160	170	180
m904.pep	190	200	210	220	230	240
	CARQTVGRGNEGISAVVDVQQRTRLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR					
a904	RAGEAVGRSNEGVSAVVDVQQRTRLRAFQKQFFAVFVFFVQHAGHVGNNRRNARRDFFDNR					
	190	200	210	220	230	240
m904.pep	250	260	270	280	290	300
	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFVFVGRADAAAGR					
a904	HHVFRFHLRGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHFVFVGRADAAAGR					
	250	260	270	280	290	300
m904.pep	310	320	330	340	350	360
	ADFAFAAXIFAGLVERDVVRQDORAGRRDFQTAFDVFHACRVQLVDFAQQFGGDDNART					
a904	ADFAFAARCFSGLVERDVIRQDORAGRRDFQTAFDVFHACRVQLVDFAQQFGGDDNART					
	310	320	330	340	350	360
m904.pep	370	380	390	400	410	420
	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC					
a904	DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC					
	370	380	390	400	410	420

430

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| |||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

g906.seq not found yet

g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTT
51  GTTGGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTGGGAAT
101 TGAATAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFGG FKNPNWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCTT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGCA AGATTCTGCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKAGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCTT
51  GTTGTGTGCC GCCGGTGGCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGCA AGGTTCTGCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTktGG AAAAATACTA TCGGCAAAAC GGCGCACAAAC
451 CTGTTGCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKAGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

```

      10      20      30      40      50      60
g907.pep  MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          |:|||||||||||||||||:|||||||||||||||||:|||||
m907      MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          10      20      30      40      50      60

      70      80      90     100     110     120
g907.pep  VFDNPKEGERWLSAMSARLARFVPEDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY
          |||:|||||||||||||||||:|||||||||||||||||:|
m907      VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          70      80      90     100     110     120

g907.pep  RARIIS
          |  |
m907      RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL
          130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCT
51  ATGTGTGCT GCGGCGCGC TGTTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTCGGCA GCATAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTTGG AAAAATACTA TCGGCAAAAC GGCGCACAAAC
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

```

      10      20      30      40      50      60
m907.pep  MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          |:|||||||||||||||||:|||||||||||||||||:|||||
a907      MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL
          10      20      30      40      50      60

      70      80      90     100     110     120
m907.pep  VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          |||:|||||||||||||||||:|||||||||||||||||:|
a907      VFDNPKEGERWLSAMSARLARFVPEDEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          70      80      90     100     110     120

```


1299

	70	80	90	100	110	120
m907.pep	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
a907	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
m907.pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTAGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa ttagccatT Ttagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAA YDFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPPIREQVK PDSIVYTDCY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAA YFHLRLLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPPIREQVK PDSIFYTDCY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908.pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAAYDFHRLRLXLIYQNGPHLEMF

```

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHRRLRLLIYQNSPHLEMPD	10	20	30	40	50	60
		70	80	90	100	110	120
g908.pep	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK						
m908	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPIIREQVK	70	80	90	100	110	120
		130	140	150	160		
g908.pep	PDSIVYTD CYRSYDVLDVSEFSHF SFAETSFSYQSQHTFCRTTKPYX						
m908	PDSIFYTD CYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX	130	140	150	160		

```

a908.seq
1  ATGAGAAAAA  GTCGCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTGCGA  GGTGTAACGT  CAAGAACGCG  AGCAGAGTTA  GTAGGCGGTA
101 ATAAAAAATC  CGCAGCGCTAT  TATTTTCATC  GTTTACGATT  ACTTATTTAT
151 CAAACAGCTC  CGCATTTGGA  AATGTTTGAT  GCGCAAGTAG  AAGCAGATGA
201 AAGTTATTTT  GGCGGACAAC  GCAAGGCGAA  ACGCGGTCGC  GGTGCTGCCG
251 GTAAAGTCGC  CGTATTCGGT  CTTTGAAGC  GAAATGGTAA  GGTTTATACG
301 GTTACAGTAC  CGAATACTCA  AACCGCTACT  TTATTTCTTA  TTATCCCGTA
351 ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATGTGTTA  CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA  TTTAGCCATT  TTAGCTTCGC  TGAAACTTCG
451 TTTTCGTATC  AATCAGACGA  CACATTTTGC  CGAACGACAA  AACCATATTA
501 A

```

```
a908.pep
      1  MRKSRLSOYK QNKLIELFVA GVTARTAAEL VGVNKNTAAY YFHLRLLIY
     51  QNSPHLEMFDF GEVEADESYF GGQRKGKGRG GAAGKVAVFG LLKRNKGKVT
    101  VTPVNTQTAT LFPIIREQVK PDSIVYTDY RSYDVLVRE FSHFSFAETS
    151  FSYQSQTFC  RTTKPY*
```

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLIELFVTGTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMF					
a908	MRKSRLSQYKQXKLIELFVTGTARTAAELVGVNKNNTAAYYFHLRLLLIYQNSPHLEMF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK					
a908	GEVEADESYFGGQRKGKRGGAAGKVAVFGLLKRNGKVYTVTPNTQTATLFPPIIREQVK					
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX					
a908	PDSIVYTDYRSYDVLDVREFSHFSFAETSFSYQSQHTFCRTTKPYX					
	130	140	150	160		

```

1   atgcgtaaaaa ccgctacttat cCTgaccatc tccgcgcgcc ttttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```

1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
 201 caaccaaag cgggggaagc ccgcgacgag gagagccgca acgtgggga
 251 aaccgagttt ccgggagagg gacggggggg ggcgggtgaa cagggcagaa
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
 51 KKVDCDEYGG ERRAVLNRQK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
 101 TGEGRKSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTGCGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AACCAGAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR			
			::	::		:
g909	ERRAVLRNQK	RGKPATRRAA	TLGKPSFRAR	DGGGRVNRAE	TGEGRKSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTGCGGG
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFILILMT AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
 51 KNNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNNMNYNQYRP
		:	:	:	:	:
a909	MRKTFILILMT	AAALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQ	TGNNADEE	HRQHWQKPKFQNRX
a909	ERHAVLPNQ	TGNNADEE	HRQHWQKPKFQNRX
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGTGCCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAFAAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAATAFAG	DSAERQIYGD	PHFEQNRTKAVKMLEQ	RGYQVYD	VDDADDYW	
m910	MKKLLLAADVSLSAAAFAAG	DSAERQIYGD	PHFEQNRTKAVKMLEQ	RGYQVYD	VDDADDHW	
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVL	SYPDLKIIKEQLDRX				
m910	GKPVLEVEAYKDGREYDIVL	SYPDLKIIKEQLDRX				
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAAACAGC CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
51 VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAE	RQIYGD	PHFEQNRTKAVKMLEQRGYQVYD
a910	MKKLLLV	AVVSLS	AATAFAG	DSAE	RQIYGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYKD	GREYDIV	LSYPDL	KIIKEQL	DRX
a910	GKPVLE	VEAYKD	GREYDIV	LSYPDL	KIIKEQL	DRX
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATT TCGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTTGATT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAAGT
401 CTGCAATGGT TCTGAAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATT TCGCGACATC
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAAGT
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          |||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAGA ACATATTGGA ATTTTGGGTC GGA CTGTTTCG TCCTGATTGG
51  CGCGGCGGCG GTTGCCCTTC TCGCTTTC CGTGGCCGCG GGTGCGGCGT
101 TCGGCGGTTT GGACAAAAC TACGCCGTT ATGCCGATT CGGCGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGC TATTGGTCGG
201 GCGCGTCGCG GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCA GTT
401 CTGCAATGGT TCTGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFVAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          |||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

q912.pep

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEI IKAK GIDGLIAELK AKNGGK*

```

m912.seq

1	ATGAAAAAA	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTGTAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCTA	TGCATTCC	TATTTGCAAT	TCCAACGTAT
201	GACCGCATCG	GCGGTCGCA	ACCTTTGGCG	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTA	AAACGCCAAC	GTCACACGTA	AAGACATCC
351	CATCGTCAAT	AAAGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TACCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
451	GGTAAATACC	GTACCTACAA	CGTCGCCATT	GAAGGCGCGA	GCCTGTTTAC
501	CGTGATCCGC	AACCAATTCC	CGCAAAATAT	CAAAAGCGAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	CGGGCAATA	A

m912.pgp

1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVP GQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

g912/m912

	10	20	30	40	50	60
g912.pep	VKKSSFISALGIGILSIGMAFASPADAVGQIRONATQVLTILKSGDAASARPKAEAYAVP					
m912	: : : : : : : : : : : : : : : :					
	10	20	30	40	50	60
	MKKSSLISALGIGILSIGMAFAAPADAVSQIRONATQVLSILKNGDANTARQKAEAYAIP					
	70	80	90	100	110	120
g912.pep	YFDFFQRM TALAVGNPWRTASDAQKQALAKEFQTLLIRTSYGTMLKFKNATVN NVKDNPIVN					
m912	: : : : : : : : : : : : : : :					
	YFDFFQRM TALAVGNPWRTASDAQKQALAKEFQTLLIRTSYGTMLKLKNANVN NVKDNPIVN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI I KAK					
m912	: : : : : : : : : : : : : : :					
	KGGKEII VRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI I KAK					
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

m912
 |||||
 GVDGLIAELKAKNGGKX
 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq
 1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
 51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
 101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
 151 CGCCAAAAAG CCGAAGCCTA TGCATTCCG TATTTCGATT TCCAACGTAT
 201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
 251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCAG CACCTATTCC
 301 GGCACGATGC TGAAATTAAT AAACGCCAAC GTCAACGTCA AAGACAATCC
 351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
 401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
 451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
 501 CGTGTAACGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
 551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep
 1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
 51 RQKAEAYAI P YDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRTYS
 101 GTMLKLK N AN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG
 151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*

m912/a912 98.0% identity in 196 aa overlap

	10	20	30	40	50	60
m912.pep	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAI P					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAI P					
	10	20	30	40	50	60
m912.pep	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLK N AN VNVKDNPIVN					
a912	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLK N AN VNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLK N AN VNVKDNPIVN					
a912	YDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRTYSGTMLKLK N AN VNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI IKAK					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI IKAK					
	130	140	150	160	170	180
m912.pep	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI IKAK					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYR NQFGEI IKAK					
	130	140	150	160	170	180
m912.pep	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq
 1 atGAAAAAAA CCGCCTACGC CATCCTCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
 101 GCGCGGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
 151 GCGCGCGCGG GCTACCGCAA AGTTACGCGG AAACCCGTCC GCGCCGGCGT
 201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAGTTT GGCAGCAATA
 251 TCTTGCGTTT GGAcATCAAA cgcgCAAGcg aAGACctcgT CCGcgteggc
 301 atCAATACCA CCTTCGGTTT GGcgGGCTC ATTGATATTG CCGGcgGgGg
 351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgTGGG
 401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccctg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTc CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

g913.pep

```

1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

m913.seq

```

1 ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTCGCGCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAACAATA
251 TCTTTCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CCGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTGTC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGGCGGCGAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

m913.pep

```

1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVAP KPVVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

	10	20	30	40	50	60
g913.pep	MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP					
	:					
m913	MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP					
	:					
	70	80	90	100	110	120
g913.pep	KPVVRAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP					
	:					
m913	KPVVRAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	:					
	70	80	90	100	110	120

1308

```

      130      140      150      160      170      180
g913.pep  DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT
          |||||
m913      DNKNTLGDTFASWGWKNSNYFVLPLVLPSTVRDALGTGITSVYSPKNIVFRTFVGRWGTT
          |||||

      190      200      210      220      230      240
g913.pep  AAAAVSTREGLLDLTDLSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL
          ||::|||
m913      AVSAVSTREGLLDLTDLSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL
          |||||

      190      200      210      220      230

      250      260      270
g913.pep  VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX
          |||||
m913      VESAETGAAETAQEDSVSETQAEAAGEAETQPGTQPX
          |||||
240      250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTT CAAATTCAAC GACCAAGCCG ACCGTACAT TTTCGCCCTT
151 GCGCGCGCGG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAGCAATA
251 TCTTGCCTT AGACATCAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGAAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAATAACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPLVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDLSLE
201 AAIKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*

```

m913/a913 100.0% identity in 275 aa overlap

```

      10      20      30      40      50      60
m913.pep  MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP AARGYRKVAP
          |||||
a913      MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP AARGYRKVAP
          |||||

      10      20      30      40      50      60

      70      80      90      100     110     120
m913.pep  KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP
          |||||
a913      KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTTFGLGGL IDIAGAGGIP
          |||||

      70      80      90      100     110     120

      130     140     150     160     170     180
m913.pep  DNKNTLGDT FASWGWKNSNY FVLPLVLPST VRDALGTGITSVYSPKNIVFRTFVGRWGTT
          |||||
a913      DNKNTLGDT FASWGWKNSNY FVLPLVLPST VRDALGTGITSVYSPKNIVFRTFVGRWGTT
          |||||

```

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCG
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGag cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGTG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTTCACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGTATG TTTTGGGCAG GTCGATTTGG
601 CTGGTGTCGC CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTCAG
651 GAACATTTTC ATTTGTTCGG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEDA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng)
 from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRCFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRCFDXCIGWTDKETDTD					
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRCFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRCFDXCIGWTDKETDTD					
	70	80	90	100	110	120
g914.pep	120 130 140 150 160 170					
m914	120 130 140 150 160 170					
	130 140 150 160 170 180					
g914.pep	180 190 200 210 220 230					
m914	180 190 200 210 220 230					
	190 200 210 220 230 240					
g914.pep	240					
m914	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTCGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTCTG
451 TAGGCTTCGA CGATTTTTCG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCAGCGG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCAATTTGT TCGGGCGTGG TGTTCGCGC TTCGTCGAGG ATGATGTATG
701 CGCGTTGAG CGTCTGCCG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEEA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFNPDL MFLGRSIWL
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
```

m914/a914 98.4% identity in 244 aa overlap

```

      10      20      30      40      50      60
m914.pep  MKKCILGILTACAAMP AFADRIDGLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC
          |||||
a914      MKKCILGILTACAAMP AFADRIDGLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m914.pep  SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD
          |||||
a914      SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--
      70      80      90     100     110

      130     140     150     160     170     180
m914.pep  TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTL
          |||||
a914      TELGFRICFSLPDFPCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTP
      120     130     140     150     160     170

      190     200     210     220     230     240
m914.pep  CSFSRASFPDLMLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
          |||||
a914      CSFSRASFPDLMLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
      180     190     200     210     220     230

m914.pep  LPRIX
          ||||
a914      LPRIX
          240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

```

g915.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacgcccc
151 aaagcccaga ttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

```

g915.pep
1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

```

m915.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCCG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng)

from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					
g915	DQPVWFSTVQMFYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCCTT ACCCCGGCAG ATTAGCGACC
 101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
 151 AAAGCCCAGA TTTTCTTGAA CGGCAAAACC GATCAGCCCG TTTGGTTCTC
 201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
 251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
 451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
 151 VVGFDMPDT YIFK*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccgca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCTT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CTGCGTAAC AATCGGTTTC
751 GCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTATGA TGCCGAAAGA GGCCTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCGC GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKFK QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGD LNIARR ABEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTGACCCCGG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CTGCGTAAC AATCGGTTTC

```

1314

```

751 GCGCGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAATAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGCGC GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDQWDLV FDPEYTSKLK QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLK					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNSFIMVPIQPA					
	310	320	330	340	350	360

370

1315

m917.pep ALKFMVRQWQDVKAGKX
 |||||
 g917 ALKFMVRQWQDVKAGKX
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq
 1 ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACAGC
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
 101 ACCGAAACGT ATTGAAATAT TACAACTGGT CGGAATACGT CGATCCGGAA
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAAATCTG
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAAG
 301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCGGCCACG
 401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
 501 GGATTGTTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
 651 CGCCTTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
 701 GCTTTATCGA TGATTGCGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
 751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
 801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCTG GATTCGAAA GATGCGAAA ACCTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
 1051 AGCTTTATCA TGGTGCTTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
 51 TVADFEKNG IKVTYDVYDS DETLESKVLTKSGYDIVAP SNAFVGRQIK
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
 151 ERVKKALGTD KLPDQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
 251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
 301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep						
a917						

1316

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a917      QCGISYLD SAAEIYPMVLN YLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
          190      200      210      220      230      240

          250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMM PKEGVGIWVDSFVI PKDAKNVANAHK
          |||||||
a917      RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMM PKEGVGIWVDSFVI PKDAKNVANAHK
          250      260      270      280      290      300

          310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFV TYAPSSKPA RELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
          |||||||
a917      YINDFLDPEVSAKNGNFV TYAPSSKPA RELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
          310      320      330      340      350      360

          370
m917.pep  ALKFMVRQWQDV KAGKX
          |||||||
a917      ALKFMVRQWQDV KAGKX
          370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51  CctegCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTC AAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 Cagggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCTGCCG CTGCCTGCCG GTTTCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTGGAaggAA GCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCGgcgTT GACGGCAAg cccCATCCT CggttacgcC
751 GAagaccCG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAACCCCG tcgggcaaat acatCCGcAt cgggTaccgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctata TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGVPVGLG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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1	ATGAAAAAAT	ACCTATTCCG	CGCCGCCCTG	TACGGCATCG	CGCCGCCCAT
51	CCTCGCGCCG	TGCCAAAGCA	AGAGCATCCA	AACCTTTCCG	CAACCCGACA
101	CATCCGTCAT	CAACGCGCCG	GACCGGCCGG	TGCGCATCCC	CGACCCCGCC
151	GGAACGACGG	TCGGCGGGCG	CGGGGCCCGT	TATACCGTTG	TACCGCACCT
201	GTCCCTGCCC	CTGTGGCGGG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCTT
251	TCCGCTCGG	CTGCGCCAAT	TTGAAAAAAC	GCCAAGGCTG	CGAGGATGTG
301	TGCGCCCAAG	CCTTTCAAAC	CCCCGTCCAT	TCCTTTCAGG	CAAAACAGTT
351	TTTTGAACGC	TATTTACAGC	CGTGGCAGGT	TGCAGGCAAC	GGAAAGCCTT
401	CCGGTACGGT	TACCGGCTAT	TACGAACCGG	TGCTGAAGGG	CGACGACAGG
451	CGGACGGCAC	AAGCCCGCTT	CTTCGATTTAC	GGTATTCCCC	ACGATTTTTT
501	CTCCGTCCCC	CTGCTGTCCG	GTTTCCGGAG	CGGAAAAGCC	CTTGTCGCGA
551	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGGCGGCACA
601	CATACGCGCG	ACCTCTCCcG	ATTCCCCATC	ACCGCGCGCA	CAACAGCAAT
651	CAAAGGCAGG	TTTGAAGGAA	GCCGCTTCTT	CCCTACCAC	ACGCGCAACC
701	AAATCAAACG	CGGCGCGCTT	GACGGCAAAG	CCCCGATACT	CGGTTACGCC
751	GAAAGCCCTG	TCGAACCTTT	TTTTATGCAC	ATCCAAGGCT	CGGGCCGTCT
801	GAAAAACCCG	TCCGGCAAT	ACATCCGCAT	CGGCTATGCC	GACAAAAACG
851	AACATCCyTA	CGTTTCCATC	GGACGCTATA	TGGCGGATAA	GGGCTTACCT
901	AAACTCGGAC	AAACTCCAT	GCAGGGCATT	AAGTCTTATA	TGCGGCAAAA
951	TCCGCAACGC	CTCGCCGAAG	TTTTGGGTCA	AAACCCAGC	TATATCTTTT
1001	TCCGCGAGCT	TGCCGGAAGC	AGCAATGACG	GCCCTGTCGG	CGCATCTGGG
1051	ACGCCCTGTA	TGGGGGAATA	TCGCGGAGCA	GTCGACCGGC	ACTACATTAC
1101	CTTGGGTGCG	CCCTTATTTG	TCGGCACCCG	CCATCCGGTT	ACCCGCAAAG
1151	CCCTCAACCG	CCTGATTATG	GCGCAGGATA	CCGGCAGCGC	GATTAAAGGC
1201	CGGGTGGCGG	TGGATTATTT	TTGGGGATAC	GGCGACGAAG	CCGGCGAACT
1251	TGCGCGGCAA	CAGAAAACCA	CGGGATATGT	CTGGCAGCTC	CTACCCAACG
GTATGAAGCC CGAATACCGc CGQTAA					

m919.pep

1	<u>MKKYLFR</u> AAL	<u>YGIAAA</u> ILAA	CQSKSIQTFF	QPDTSVINGP	DRPVGIPDPA
51	GTTVGGGGAV	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAQFTPVH	SFQAQKFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDDR
151	RTAARAFPIY	GIPDDFISVP	LPAGLRSGAK	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPHY	TRNRQINGAL	DGKAPILGYA
251	EDPVLEFFMH	IQQSGRLKTP	SGKYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	KLGGTSMQGI	KSYMQRNPQR	LAELVGQNPV	YTFPRELASS	SNDGPGVAGL
351	PTPLMGSEYAGA	VDRHYYTLGA	PLFVATAHPV	TRKALNRRLM	AQDTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVVQL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/q919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQP	PDTSVINGPDRPVGIPDPAGTTVGGGGAV				
	: : :	: : :	: : :	: : :	: : :	: : :
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFFQP	PDTSVINGPDRPAGIPDPAGTTVAGGGAV				
	10	20	30	40	50	60

	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
	: : :	: : :	: : :	: : :	: : :	: : :
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVLEFFMHIQSGRLKTPSGKYIRIGYADKNEHPVVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVLEFFMHIQSGRLKTPSGKYIRIGYADKNEHPVVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGVPVAGLGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVAGLGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCCG CGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCTCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGCCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCTCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGCGGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

```

1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT
 1251 TGCCGCAAAA CAGAAAACCA CCGGATATGT CTGGCAGCTT CTGCCCAACG
 1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTAQAQFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNP YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
              10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
          |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
              70      80      90      100     110     120

              130     140     150     160     170     180
m919.pep  YFTPWQVAGNSLAGTVTGYEYEPVLKGDGRRTAQAQFPIYGIPDDFISVPLPAGLRSGKA
          |||||
a919      YFTPWQVAGNSLAGTVTGYEYEPVLKGDGRRTAQAQFPIYGIPDDFISVPLPAGLRSGKA
              130     140     150     160     170     180

              190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
              190     200     210     220     230     240

              250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
              250     260     270     280     290     300

              310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPORLAEVLGQNPYIIFRELAGSSNDGPVGALGTPLMGEYAGA
          |||||
a919      KLGQTSMQGIKAYMQQNPRLAEVLGQNPYIIFRELTGSSNDGPVGALGTPLMGEYAGA
              310     320     330     340     350     360

              370     380     390     400     410     420
m919.pep  VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||||
a919      VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
              370     380     390     400     410     420

              430     440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
          |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
              430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al, 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCccgcgca caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGcgcmaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttctc
551 CCGATcaaaG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY OPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCT
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEPPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YOPTFFSKXX AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920 .pep				PMQLVTEKGKENMIQRGT	YNYQYRSNR	PVK
m920	GGEYLKADLGYGEFPELEPIAKDRLHIFSKPMQLVTEKGKENMIQRGT	YNYQYRSNR	PVK			
	40	50	60	70	80	90
g920 .pep	DGSYLVTAIEYQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
m920	DGSYLVIAIEYQPTFWSKKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT					
	100	110	120	130	140	150
g920 .pep	KPVGQNLEIVPLDNPADIVHVGXRFKVRVLFGRGEPLPNATVTATFDGFDTS	SDRSKTHKTEA				
m920	KPVGQNLEIVPLDNPANIHVGERFKVRVLFGRGEPLPNATVTATFDGFDTS	SDRSKTHXXEA				
	160	170	180	190	200	210
g920 .pep	QAFSDTTDGEGEVDIIPLRQGFWKASVEYKADFPDQSLCRKQANYTTLT	FQIAHSHHX				
m920	QAFSDSTDDKGEVDIIXLRQGFWKANVEHKTDFFDQSVKQKQANYSTLT	FQIGHSHHX				
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920 .seq

```

1  TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCACGCC CACCGCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAACA ATGCCTGACG CAAGCTATTG CGAACAACCC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGACAAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920 .pep

```

1  *KKTLLTLLAV SALFAASAHV HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFFDQSVK
251 QKQANYSTLT FQIGHSHH*

```

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLLLSVSALFATS	SAHAHRVWVETAHT	HGGEYLKADL	GYGEFPELEPI	AKDRLHIFS	
a920	: :	: :	: :	: :	: :	: :
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMI	QRGTYNYQYRSNR	PVKDGSYLVIAEY	QPTFWSKXKAGW	KQAGIKE	
a920	: :	: :	: :	: :	: :	: :
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFG	KNIVNVGHESADT	AIITKPVGQNLEI	VPLDNPANIHV	GERFKVRVL	
a920	: :	: :	: :	: :	: :	: :
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTAT	FDGFDTSDRSKTH	XEAQAFSDSTDD	KGEVDIIXLRQ	GFWKANVEH	
a920	: :	: :	: :	: :	: :	: :
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQ	ANYSTLTFQIGH	SHHX			
a920	: :	: :	: :			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCTCCGA ACTCGAACCC
151 ATCGccAAAG ACCgctTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTCCCGTTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCC
401 GTAAAAACAT TGTCACCGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCGT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTGACGCG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGC GC CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 QKQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCCC CACCgCGTCT GGGTCGAAAC CGCCACACAG CACGCGGCGG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCTCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```


1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAATACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1  MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTERG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/g920-1 96.3% identity in 268 aa overlap

          10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          |||
g920-1      MKKTLTLLAVSALFATSAHPRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          10      20      30      40      50      60

          70      80      90      100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
          |||
g920-1      KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE
          70      80      90      100     110     120

          130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
          |||
g920-1      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
          |||
g920-1      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIIPLRQGFWKASVEY
          190     200     210     220     230     240

          250     260     269
m920-1.pep KTDFFDQSVCKQKQANYSTLTFQIGHSHHX
          |::|
g920-1      KADFFDQSLCQKQANYTTLTFQIGHSHHX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1  TGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCGTCT GGTTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAATACTC GACTTTAACC TTCAAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

      10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920      XXXKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90     100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
a920      KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQONLEIVPLDNPANIHVGERFKVRVL
a920      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQONLEIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep KTDFFPDQSVCKQKQANYSTLTFQIGHSHHX
a920      KADFPDQSVCKQKQANYSTLTFQIGHSHHX
      250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMKMQP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```

m921.ppt

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLESS
51 HWTDAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 ELMEVMKMQP LK*

Homology with a predicted ORF from *N.gonorrhoeae*

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFR	LASSHWTVDVAKI	SD			
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFR	LAPSHWADVAKI	SD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYL	RS	AID	SQ	RGA	INTEQ
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYL	SAVD	SQ	RGE	INTEQ	
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNNMDVKPNNPAFTNFLMEVMKMQPLKX					
g921	SKLYIENALRGWQQRWKNNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

a921.seq

1	ATGAAAAAT	ACCTTATCCC	TCTTTCATT	GTGGCAGTTC	TTTCCGGCTG
51	CCAGTCTATT	TATGTGCCCA	CATTGACGGA	AATCCCCGTG	AATCCTATCA
101	ATACCGTCAA	AACGGAAGCA	CCTGCAAAAG	GTPTCCGCCT	TGCTCTTCG
151	CATTGGACGG	ATGTTGCCAA	ATGACGCGAT	GAAGCGACGC	GCTTGGGCTA
201	TCAGGTGGGT	ATCGGTAAAA	TACCAAGGT	TCAGCGGGCG	CAATATCTGA
251	ACAACTTCAG	AAAACGCTG	GTCGGACGCA	ATGCCGTGCA	TCGACAGTATG
301	TATGAAATCT	ACCTGCGTTC	GGCGATAGAC	AGCCAGCGGG	GCGCAATCAA
351	TACGGAACAG	TCCAAGCTGT	ATATCCAGAA	TGCCTTCCGC	GGCTGGCAGC
401	AGCGTTGGAA	AAATGTGGAT	GTCAAACCCA	ACAACCCCGC	ATTTACCAAC
451	TTTTTGATGG	AAGTGATGAA	GTCCAGCCCC	TGAAATGA	

a921.pap

```

1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLLASS
51 HWTDAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMQP LK*

```

m921.pep MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a921 MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
 10 20 30 40 50 60

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	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVKQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVKQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTCC CAGGCGAAT
251 GGCAGGATTT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAaA
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAAt acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAA GAATTGTCG AGCTTTTAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGtcgg tgatgtcgcg
751 gcatcggTTG CCAATTAtat gaagCAGCAC GGTTGGCGCA Cgggcggtaa
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGACGG TGGCGGATTT GAaggCGTAc
901 ggcacatcc ccgggaaac GCTCGCAGAT GATGAAAGg cgGTTTTGTT
951 CAACTGGAA ACCGCACCCG GCGTGTGTA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGATGTA TGTAAACGgcg
1051 gtcaggGACA TTGCAATTC GTCGCGCGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVKGDFS QAEWQDFDQ AAYKADIVKI
101 MHRPSTSRPW YVFRGNNGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFQ YPRRAGFFQK ELVELLKLAK
201 EEGDVVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRGTGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYIL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGACATCG TCAAGATTAT GCACCGCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATT CGGGCAAGG GAAATTTCG GCGCGCGCC
401 GGTTTTATGC GGAAACCGC GCGTTATCG ATGATGTGGC GCAAAATAC
451 GGCGTGCTG CCGAACTTAT CGTGGCGTT ATCGGATTG AAACGAATTA
501 CGGCAAAAT ACGGGCAGT TCCGTGTGGC GGACGATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGTTTT TCAAAAAGA ATTGGTCGAG

```

```

601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCAGC GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GCGGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCAGATGA
951 TGAAAAGCGC GTTTTGTTC AACTGGAAAC CGCACCGGGC GTGTTTGAAT
1001 ATTATTTGGG CTGAAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

-- This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

```

m922.pep
1  MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKEsrpafda
51  AAVFDAAAVP VSDSGFAANA NVRRFVDEV GKGDfsraew QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SsyRkwaVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

```

m922.pep      10      20      30      40      50      60
               MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKEsrpafdaAAVFDAAAVP
g922           10      20      30      40      50
               MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKEsrpafdaA-----AVP

m922.pep      70      80      90      100     110     120
               VSDSGFAANANVRRFVDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
g922           60      70      80      90      100     110
               VSDSGFAANANVRRFVDEVGKGDfsraewQDFFDKAAYKADIVKIMHRPSTSRPWYVFR

m922.pep     130     140     150     160     170     180
               TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL
g922          120     130     140     150     160     170
               TGNSGRAKFGHARRFYAENRAVIDDVAQKYGVPaelivavIIGIETNYGKNTGSFRVADAL

m922.pep     190     200     210     220     230     240
               ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSyRkwaVDY
g922          180     190     200     210     220     230
               ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSyRkwaVDY

m922.pep     250     260     270     280     290     300
               DGDGHRDIWGNVGDVAASVANymkQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV
g922          240     250     260     270     280     290
               DGDGHRDIWGNVGDVAASVANymkQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV

m922.pep     310     320     330     340     350     360
               ADLKAYGIIPGEELADDEKAVLfkLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
g922          310     320     330     340     350     360
               ADLKAYGIIPGETLADDEKAVLfkLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI

```

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	300	310	320	330	340	350
		370				
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTTGTG
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCCTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGCAAAAGA AGAAGCGGCG GATGTTTTCG CCTTTAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCG GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGCGTACGG CATCATCCCC GCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTGTTC AACTGGAAAC CGCACCAGC GTGTTTGAAT
1001 ATTATTTGGG CTGAAACAAT TTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDPYPR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GKKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKESRPAFDAAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
m922.pep	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	190	200	210	220	230	240

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```

m922.pep  ATLGFDPYPRRAGFFQKELVELLLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
a922      ATLGFDPYPRRAGFFQKELVELLLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGKLTALTRTV
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGKLTALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLEFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
a922      ADLKAYGIIPGEELADDEKAVLEFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTGGACG GCGCATACT TGGGTAGTAG GATGTTTCTG CATAAAACGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCG AACTTTTTGT
351 AAAACTCGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGRSMFR HKTAKKRFV LFRLLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCCTG CCTTGCCGTA CTATTGTGAC TGTCTGCGGC TTCGTCGCCT
401 TGTCTGATT TTGTTAATC CACTATAT.T ATTTGTGCCC GCCTGAATTT
451 TTCGTAAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAIR
51  GORRIPEHRL LLPALLGGWV GAYFGSMTEK HKTAKKRFV LFRLLTVSGNV
101 LATLILISG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

1	ATGAAGCGGC	AGGCTTTCTT	CAAACATGATG	GCGTGTGCGG	CATTTCTGTC
51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTAC	GCAATATTGT
101	CCCTCTATGC	GTTTGCACTT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
151	GGAAAACGCC	GCATTCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCCG
201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
251	CGAAAAGCG	TTTTGTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TAAATTTAA	ACCAGTACGG
351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
401	ACCAAGTGAA	TCGGTCCCGT	ACTATTGTGA	CTGCTGCGG	CTTCGTCGCC
451	TTGTCCTGAT	TTTTGTAAAT	CCACTAT.AT	TATTTGTGCC	CGCCTGAATT
501	TTTCGTAAAA	CTCGGCAGA	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
51	GKRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFV	LFRLTVSGNV
101	LATLILIIYS	GNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRRTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcgcggtgt TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgaggggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCCTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKGPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGCGGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKCKGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGCGGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGA AAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

```

m925-1.seq
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTTCA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

```

m925-1.pep..
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51  NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMDKI IAHQKKCGQT AQAYRDARNA LPSNQTYYQH LAIEQLKRR
151 FEAEFDELEK EIKCNRSPPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGE					
	10	20	30	40	50	
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQHLAAIEQLKRRFEAEFDELEKEIKCNRSPPALLX					
	120	130	140	150	160	170
g925-1	AQAYLDARNALPSNQTYYQQRQAIEQLKRRFEAEFDELEKEIKCNK-PTLLFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

```

a925-1.seq
1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTTCA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTCAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

```

a925-1.pep
1  NKINVFTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMDKI IAHQKKCGQT AQAYLDARNA LPSNQTYYQH QAAIEQLKRR
101 FEAEFDELEK EIKCNKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
	30	40	50
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTKGEESMLLSEKDGALSINTGIGE		
	40	50	60
	60	70	80
	80	90	

1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
              |||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
              90      100      110      120      130      140

              100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
              |||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
              150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCGTGG AAACCATCAA
201 TATCAACACC CTTTGGGCA GTACGCTCGG ACAGTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgccGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCGTGG AAACCATCAA
201 TATCAATACC CTTTGGGCA GTACGCTCGG GCAGTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCAGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSGQVRTL QLNNGNLIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

              10      20      30      40      50      60
g926.pep      MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              |||
m926           MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
              10      20      30      40      50      60

              70      80      90      100     110     120
g926.pep      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
              |||
m926           PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRQLVGFKLPIQYLHI
              70      80      90      100     110     120

              130     140     150     160
g926.pep      WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

```

```
a926.pep
1  MKHTVSASVI  LLLTACAQLP  QNNENLWQPS  EHTRSFTAEG  RLAVKAEGKG
51  SYANFDWTYQ  PPVETININT  PLGSTLGQLC  QDRDGALAVE  GKGNVYQAES
101 AEELSRQLVG  FKLPIQYLHI  WADGRPVAGA  PYRILPDGIL  EQYGWTVGRT
151 ADSGGQVRTL  QLNNGNLNR  LVFEIGMPS  ETETOEOCAA  RIO*
```

		10	20	30	40	50	60
m926.pep		MKHTVSASVILLTACAQLPQNNENLWQPSEHIS	SSFAAEGRLAVKAEGKGSYANFDWTYQ				
a926		MKHTVSASVILLTACAQLPQNNENLWQPSEH	TRSF	TAEGRLAVKAEGKGSYANFDWTYQ			
		10	20	30	40	50	60
		70	80	90	100	110	120
m926.pep		PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESA	EELSRQLVGF	KLPIQYLHI		
a926		PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESA	EELSRQLVGF	KLPIQYLHI		
		70	80	90	100	110	120
		130	140	150	160	170	180
m926.pep		WADGRRVAGAPYRILPDGILEQYGWT	VGRTADSGGQV	RTLQLNNGNLN	IRLVFTEIGMPS		
a926		WADGRPVAGAPYRILPDGILEQYGWT	VGRTADSGGQV	RTLQLNNGNLN	IRLVFTEIGMPS		
		130	140	150	160	170	180
		190					
m926.pep		ETETPERCAARTRX					
a926		ETETQEQAARIQX					
		190					

g927.seq

```
1 atgaaaacct acGCacAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51 CAGCCCcgca GCcgatTcaa accaTCCGTC CGGacAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtacc TGctcaatgc cTcgtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcgaaCATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACA TCCACGCGC
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGATCATGCAC ATGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCAGCCG GCACCTTACA
```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CTTCTCTCGG CGCATAACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAACTCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAY YGLKANNGNE QEAQKLVASI
201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGGAATA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCAGGGG ATTTTACAA AGAATAACA CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCCTT CTTGGCGCA TACGGTTACG
551 GTCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCCATCCTCA AAAACACCCC CGTTTTGAA AACGGCGGAC GCKcGCCACC
651 ACCACCTTCA CACAACGCAA CATCGCGGAC GTACTCATCA CTTTGAAAA
701 CGAAGCCAAC TACGTCAGCt AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLEKXGLVEK					
	70	80	90	100	110	120
g927.pep	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS
          |||||:::|||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAAACCT  ACGCACCAGG  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTGAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACC GGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCcgat TATGCagtcg attgCggCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaatCCC atttcgtcgg ctAtggctat taCTGcaact
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttcgcgtCTT TCttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccgcg
 701 ttatcgccctt TTtcgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGCTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
 1051 TTTTAAATA Aactcggact gattaaatGG TTCTCCGGAG TGTGGCGGA
 1101 AagtgtcggC GGTTCGGCGC TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
 1351 TGCTACACCA CAATGGGAGA ATGGTGAAG GCGGTTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCAV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWVK AGFIMSVVNF LIFSIVGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACC GGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

1338

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451 GGCGGCATTA TACATCCGAT TATGCACTCG ATTGCCGCGA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTTCGTCTG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCTGTATG CCTTTGATTT TATATTWYT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTGCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSP ISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACC GGCGTA ACCGCCGACA AACCGGTGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTGTGT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGTCGCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTCAA TTTGCCAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTGCGC GGTGTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTGCGCGC ATTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCTCAC TCATTATGCG ACCGTAATT CGCCTGTGAT TTTGCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGTTG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNVAV FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLA MYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMFVGVIAAIIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMFVGVIAAIIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLMRIGYLFIAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m929.pep	FGRKTLGIGY SLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGY SLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m929.pep	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m929.pep	PLILYXLYPPEIKETPNVAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
a929	PLILYFLYPPPEIKETPNVAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
m929.pep	FSGVLAESVGGGLGVSGTAAGVILVLA MYA HYMFASTTAHITAMFGAFFAAAVSLNAPAM					
a929	FSGVLAESVGGGLGVSGTAAGVILVLA MYA HYMFASTTAHITAMFGAFFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
m929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPABEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCGAG
201 ACGTATTGCA GCATTCCAAA ACAAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGCTCTCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAAACA
351 AAGTGATGTC GTGGTGCAAT GCGCGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAATATTG GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAAACA ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGAAAAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTGATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACC ACAGGTGTTG
851 TGGCAGAACT TCCCAACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAT ATAAACACGG CACCGGCATG AAAGATGCTC TCGCGCGGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAT GGTATTCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTATTTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAERDLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1 ATGAACTTC CTTATCCTA TTGCTTAAT ATTCGCTTTT TGTCTTGGT
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAA GAAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGGAAACGG GTTTTCAGGC
351 TGCCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAA TGGACGTTTC ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGCCCATC GCAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGAAAAA
1051 AGTTACAATA CTGATTTTCG CTCAACCCG CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA AAAAAAGTT
1151 ACATTGATGA TGCCGAACG ACTGTACAAC GCGCTAAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTCCACAA AGAATATATC GGTGCGAGTA CGGCAGATT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGCGGAA GGCACGTAC GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTCAAATC GGTAAACAGC TATTGCTTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGCTGATG GTAGGACATG
1601 TTTCAAGACA ATCCGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGCA GATAAAGCTT GCGCGCAAC TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAGAGCC CGAATTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1 MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL
201 LNLRLDLEQGL ENLRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGRHKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRKT YLGVKLMWRE TKS YIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTMKMDA LRAPEEAFGE GTSRMIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDE
501 MSLSAERGWI WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHA RFQFALKRAL RETGFQAGKCLHAGNINQIMSLAQNALIGR GYTTTRILAA					
g930-1.pep	:					
					10	20
						30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDLE					
g930-1.pep	:					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGL ENLRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV SVGMDSNGSE ATGKYQG					

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```

g930-1.pep  QGLENLKLCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
NITFSADNPGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLGVKLMWRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270
m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330
m930-1.pep  450      460      470      480      490      500
WTASADVNTFPQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTFPQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390
m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGAADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGAADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450
m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWTGFGVGYSEFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCTT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGCG GGACAACGGT TCGCTCGACT
401 ACAAAAACCG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGCGCG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kct TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAAT CGCCGCGGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTCTG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

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451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

-- m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNV	VPVQPVKIRR				
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNV	VPVQPVKIRR				
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPWPDAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACCGC

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```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTCAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GCGCGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTG TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQQGFHAQP
151 PKCTTGAGAG ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLGLALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAA
101 ACACCATTCG TGCCGAAGCA CAGGCAAAACG GCAACAACG GCAACCCGTT
151 ACCGGTAA .A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCTGGTC GCGCGGCGCG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 .yCAGCAGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCG
451 CCGGCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGGCGCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTtAT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRRAVYL RPIDRKLAAA KPGRRGRRV YRQAGKQIH TGRQPROSRR
101 PARACSLPSV RTPQCAHQGG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARGCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

		10	20	30			
m934.pep		RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI					
g934	MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI	10	20	30	40	50	60
		40	50	60	70	80	90
m934.pep	PAEAQANGNNGQPVTKXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR						
g934	PAQAQANGNNGQPVTKXRRRAVYLRPIDRKLAAAKPDWRGRRVYRQAGKQIHTGGQPR	70	80	90	100	110	120
		100	110	120	130	140	150


```

m934 . pep      QSRRPARACSLPSVRTPQCAHQQGFHEHAQPPCKTTGGAXAALPPDNAPXRQLPPRYARF
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g934            QPRRPSRACCLPSVRTPQCAHQQGFHEHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
              130      140      150      160      170      180

              160      170      180      190      200
m934 . pep      RQEAVNPARQCRLKSFQTAFXHLGLTLLCCRLIFRRHFVSKRLMSGWQFX
| | : | | | | | | | | | | | | : | | : | | | | | | | | | | | | | |
g934            RQKAVNPARQCRLKGFQTAFYLLGALLCCRLIFRRHFVSKRLMSGWQFX
              190      200      210      220      230

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATT CG CACTCGGCGC
51  TCGCCAAGAC GACGGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGC GACAGCATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG. TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGGACGGAAG CTGCGTGTCT CAAAGCCTGG TCGGCGCGCG
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATT AC ACAGGCGAG
351 GCAACCAAGA CAGTCCCGTC GCCCGGCGCG CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACGACGAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGCGCG GCAGGCGCGA CGGTTACCGC CGGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TCGCGGGTTT CGGCAGAAGG
551 CGGTAATATC GGGCTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATTT
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTCCT AAGAGTTTGA TGTGCGGGAT GCAATTCTGA

```

a934.pep

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AAQADDTVYQ
51	LTPEAVKDTI	PAEAQANGNN	GQVPTX*RR	AVYLRPIDRK	LAQAAPGRRG
101	GRRVYQRQA	KQIHTRGQPR	QSRPRACR	LPSVRTSQCA	HQQGFHAQP
151	PKTITGGAGA	ALPPDNAPAR	QLPPRHARF	RQKAVNPACQ	CRLKGFQT <u>AF</u>
201	<u>LYLLGTLLCC</u>	<u>RLIFRRHFVS</u>	KSLMSQWF*		

```

m934.pep
10 20 30
RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
|||||
a934
MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
10 20 30 40 50 60
40 50 60 70 80 90
m934.pep
PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
|||||
a934
PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGRQPR
70 80 90 100 110 120
100 110 120 130 140 150
m934.pep
QSRRLPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
|||||
a934
QSRRLPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
130 140 150 160 170 180
160 170 180 190 200
m934.pep
RQEAVNPARQCRLKSFQTAFXHLLGTLLCCRLIFRRHFVSKRLMSGWQFX
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934
RQKAVNPACQCRLKGFQTAFLYLLGTLLCCRLIFRRHFVSKSLMSGWQFX
190 200 210 220 230

```

g935.seq not found yet

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCT GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATCGCGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CCGCCGCAA TATTGCCCGC AAAACGGAGG
651 CCGGCAGATA TGCAAGTGTA GCGGGGCGGA GCGGGGCGCA GGTTTGAATT
701 ATGAAATCGA GCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCG GTAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CCGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTCTG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGTTG
1251 GGCGCAGGAG TGGCGGCACT TGGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCGCGA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFFLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNVEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 LSGDFDAKTK RVNNRRLPPY MLAGVGTVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCT GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATCGCGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAATT
501 GGATTTGCCG GCGCCGTTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCCGGGCGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTTCG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGCTCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GCGCAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTCCCGCT
1301 CTTATGCCCC CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIA KRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
a935	MLYFRYGLVVWCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

1350

	310	320	330	340	350	360
m935.pep	GSDGFD AKTKRVNRRLLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFD AKTKRVNRRLLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWREF					
a935	GRTESNVPYAKRRNSEVFVSADWREF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgaACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

1351

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

```

      10      20      30      40      50      60
m936.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g936       MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAGVGAKSVIDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

      70      80      90     100     110     120
m936.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g936       ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90     100     110     120

      130
m936.pep  VASLPRTAXXX
          |||||
g936       VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
          130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

```

a936.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGCGGAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

```

a936.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVSAVVG AAVGAKSVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936/a936 95.3% identity in 128 aa overlap

```

      10      20      30      40      50      60
m936.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a936       MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGVGAKSAVDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

      70      80      90     100     110     120
m936.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:
a936       ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90     100     110     120

m936.pep  VASLPRTA

```

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGCGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGccgAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACCTGGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCaccgt  CGGCGTACAA  AAAGTCATTA  CCCTTACCA  AAACACGTCT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVTILYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGGGCGCGA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGGTGTACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCCGGCGAC  ATCGCCGGCG
401 ACACCTGGAA  CACATCCAAA  GTCCGCGCCA  CGCTGTGGG  CATCAGCCCC
451 GCCACACAGG  CGCGCGTCAA  AATCGTTACC  TACGGCAACG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACCGT  CGGCGTACAA  AAAGTCATCA  CCCTTACCA  AAACACGTCT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT  LIAAIFSLAL  SGCVS AVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIV  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVTILYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDDNVMALRIETT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCC
101 GCGCGAAATC CGCGCTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAGTCATCA CCCTCTACCA AAACCTACGC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTA AVL SLAL GGC VSA VVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALEIETT
              |||||
a936-1      MKPKPHTVRTLTA AVL SLAL GGC VSA VVG GAAVGA AKSAVDRRTTGAQTDDNVMALEIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTagt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCAC TTGCCT CACCGGTTTA CATT CAGACC GGCTCCGCTT CCTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAcgG GCAataccgA CATTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTGacg GCAACGGCAA

```

g937.pep

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

1	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
101	AATGGAAACT	GGAACCTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
151	GCCGAACTTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
201	CCCCATTCCG	ACGGAATATC	AAGAAAaCGG	CAGCAATACC	GATATGCTCG
251	TCGGCAGCGT	CGGTTTGGCG	TACGGATGTA	CCGGGAATAC	CGACATTTAC
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACTCG	ACGGCAACAG
351	CAAAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
401	CTTTCTCTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCCGGAA	AATCCTGGCT
501	CATCGGCGCC	ACCACCTACA	AAGCCATAGA	TCCGATTGTC	CTTTCCCTCA
551	CCGCGCGCTA	CCGCATCAAC	GGCAGCAAAA	CCCTTTTACA	CGGCATCCGC
601	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTGTCTGC
651	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GCGAGGCAGC
701	CCGACCGGAC	GGACGGCAAA	CGGAATCCT	CCAGAAACAC	ATCCACCTAC
751	GCCCATTTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
801	ATCCGACAGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTG
851	CGGTACAGCA	TACATTTTAA			

m937.pap..

1	MKRIFLPALP	AILPLSTYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSNNR
-51	AELAAPVYIQ	TGATSFIPIP	TEIQENGST	DMLVGTGLGR	YGLTGNTDIY
101	GSGSYLRWEE	RKLDGNSKTR	NKRMSDVSLG	ISHTFLKDDK	NPALISFLES
151	TVYEKSWKA	SSGKSWLGA	TTYKAIDPIV	LSLTAAAYRN	GSKTSLDGIR
201	YKSGNYLLLN	PNISFAANDR	ISLTGGIQWL	GRQPDYRTDGK	RESSRNTSTY
251	AHFGAGFGFT	KTTALNASAR	FNVSQGSQSS	LKQFVOHTF*	

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep    MKNILL-VFVSFVPLCVRTLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ
           |||:::||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m937        MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
           10      20      30      40      50      60
g937.pep    60      70      80      90      100     110     119
            TGSASFIPVPTEIQENGSNTDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTT

```


[illegible]

```

a937.seq
1  ATGAAGCGCA TCTTTTGCC CGCCTTGCC GCATCCTGC CTTTATCCGC
51  TTATGCCGAC GTGCCCTTGA CGATTGAAGA CTAATGACC GACAAGGGCA
101 AATGGAACCT GGAACCTTCC CTTACTTACC TGAACAGCA AAACAACCGC
151 GCCGAAC TTG CCGCACC GGT TTACATCCAA ACCGCGCAA C TCTCGTTTAT
201 CCCCATCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCT CCGTTTGCGC TACGGA CTGA CCGGGAATAC CGACATTTC
301 GGCAGCGCA GCTATCTGTG CACGGAAGAA CGAAACTCG ACGGCAACGG
351 CAAAACCGA AACAAACGGA TGTCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCTTAA AGACGACAAA AACCCCGCCC TAATCAGGTT TCTTGAAAGC
451 ACGGTTTACG AAAATCGCG CAACAAGGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTGCTC TCTCTATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGCAT CCAATGGCTG GGCAACGACG
701 CCGACCGTCT GGACGGCAAAA AAGAATCCG CAAGAACAC ATCCACCTAT
751 GCCCATTTG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACAGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTTAA

```

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSNNR
51	AELAAPVYIQ	TGATSFIPIP	TEIQENGSTN	DMLVLTGLGR	YGLTNGTDIY
101	GSGSYLWHEE	RKLDNGKTR	NKRMSDVSLG	ISHTFLKDDK	PNATISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSITAAYRIN	GSKTSSNTK
201	YKAGNYWMLN	PNISFAANDR	ISLTGGQIQWL	GKQFDRLDHG	KESARNSTSY
251	AHFGAGGFGT	KTALLNASAR	FNVSGGSSE	LKFGVHTF*	

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRRAELAAPVYIQ					
a937	:					
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRRAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937	:					
	70	80	90	100	110	120
	TGATSFIPIPTEIQENGSNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937						
	130	140	150	160	170	180
	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937						
	190	200	210	220	230	240
	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a937						
	250	260	270	280	290	
	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAACCGG
251 TGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGCGGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGAAGATAT TGCAAACCGT ATGCTGAAG AAGATTGAA AGCGGTCGCC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAYIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLAFVLAAGAVSASP	KADVEKGQVAATVCAACHA	ADGNSGIAMYPRLAAQHTAY			
a939						
	MKRLTLAFVLAAGAVSASP	KADVEKGQVAATVCAACHA	ADGNSGIAMYPRLAAQHTAY			

1357

```

              10      20      30      40      50      60
              70
m939.pep      IYHQTIGIRDVNAP
              |||||
a939          IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDQILNVSAFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGCG GCCGTGCGG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950          SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

```
a950/m950 100.0% identity in 102 aa overlap

      10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||

      10      20      30      40      50      60

      70      80      90     100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          |||

      70      80      90     100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGCGC AACGGGTCAA
201 CAGGGTGTTC ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTGGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GTGGCTCAA AAAGCATCGA AAGCGGTTCC CCGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCGCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAAT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGCGGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTTGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDVQ KRRIFLLLVQ AAVQOGGVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDEI LPPTLMTLRL
251 TARKYPEILD GFFEQDTQON LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKQVS APEYLFQKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLKG AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGCGGAGCG
201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAACCCGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCCG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAGG TGCTGGCTCA
501 GGCAGGAGAA GGACAGAACG GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCGC AAAAGGAAAA GGCAATCGGA GCTTTCAGC
701 GTTGGCGGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGTCTG GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTGAGG CAGCGATATT
951 GGCAGCAAA CAAAAAGAG GTGCTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GGCCTAACG
1051 CGGCGGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCCGCGC
1201 ATCGGCGAGG TCGGAAACT TCCGAAACG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTTG TCCAAATAC AGATGCTCGC CCTGTGCAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAGTTGT
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTAGAT CTTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GGCGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTCTG TTGAAAACGA CCCCAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AACGTCACG GCATCGCATT GCCCCAACCT TCCGAAAAAC CTCGGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPKVGV KVFRKQORYS
51 EEEIKNERAR LAAVGERVNO IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLRTARKYPEI LDGFFEQDTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQSRRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFQK GVLAATAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIIEKPPA
451 GSNTELQAEA LVQSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGAGDMKQPKVGVFRKQORYSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVLRKHRRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNOIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	70	80	90	100	110	
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRRERGNQHLDGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGEAQKRAGWLRNVLREGGNQHLDGLEEVLAQSDDVQKRRIFLLL					
m951.pep	190	200	210	220	230	240
	AQAAVQDGLAQKASKAVRRAALKYEHLPAAVADVVFVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEEQSRRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLEHNPANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRRAAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKVSAPEYLFDKGVLA AAAA AELDGGRAALRQIGRVRLPEQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIQLALSKLPDKREALIGLNNIIAKLSAAGSTEPLAEALAQRSIIEQFGKRGKMIAD					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCGAG GCGTATGCCG CCGGCGCGGC GGATGCCAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTCACAGA AAGCAGCAGC GTTACACCGA GGAAGAAATC
151 AAAAAACGAAC GCGCACGGCT TCGCGCAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGCGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGAGG
451 AATCAGCATC TAGACGGAAT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACAGAACCCG AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGTTTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGACGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTTC GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGGAAACG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGCGCG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAGTCA AGGCAGTGGT TGAAAAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGCGCG
1151 CTGTGAGATT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CGGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTGTTC
1251 CAAATACAGC ATGTTGCGCC TGTCGAAGCT GCCCGACAAA CGGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCTGCGCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAAATGA TTTGAGATCT TGAAGGGGCG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTGT
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CCGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGO AYAAGAADAK PPKEVGKVF R KQORYSEEEI
51  KNERARLAAV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDDGLEEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTIELP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVQOMEIIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDPEPEVAA HLGVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAG--AADAKPPKEVGKVF RKQORYSEEEIKNERAR
          ||| || :||:|:|:|:|:| ||| | :| | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEVGKVF RKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPEVAERALEMAVSLNAFE
          60      70      80      90     100     110
```

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|||||
m951      LAAGVERVNIQIFLLGGETALQKQGAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
              70      80      90      100      110      120

              120      130      140      150      160      170
a951.pep   QAEMIQKWRQIEPIPGKAQKRAWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
              |||||
m951      QAEMIQKWRQIEPIPGKAQKRAWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
              130      140      150      160      170      180

              180      190      200      210      220      230
a951.pep   AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
              |||||
m951      AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
              190      200      210      220      230      240

              240      250      260      270      280      290
a951.pep   EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              |||||
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              250      260      270      280      290      300

              300      310      320      330      340      350
a951.pep   LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD
              |||||
m951      LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD
              310      320      330      340      350      360

              360      370      380      390      400      410
a951.pep   YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQQGRYFTADNL
              |||||
m951      YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQQGRYFTADNL
              370      380      390      400      410      420

              420      430      440      450      460      470
a951.pep   SKIQMFALSKLPDKREALRGLDKIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              |||||
m951      SKIQMLALSKLPDKREALRGLDKIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              430      440      450      460      470      480

              480      490      500      510      520      530
a951.pep   LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
              |||||
m951      LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
              490      500      510      520      530      540

              540      550      560      570      580      590
a951.pep   GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWVQAAHLTGDKKIWRETL
              |||||
m951      GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWVQAAHLTGDKKIWRETL
              550      560      570      580      590      600

              600      610
a951.pep   KRHGIALPQPSRKPRK
              |||||
m951      KRHGIALPQPSRKPRK
              610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51      TTACGGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101     TTGTAAAGCA GGATTGGAT TTTTCTGCG GGGCGGCTTC GGTGGCGACG
151     CTTTTGAACA ATTTTACGG GCAAAGCTG ACGGAAGAAG AAGTGTGGGA
201     AAAACTGGGT AAGGAACAGA TGCGCGCGTC GTTTGAGGAT ATGCGGCGCA
251     TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301     CAGTCGCGCG AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351     AGACGACCAT TTTTCGGTAT TGCGCGGAGT GGATGGCAAT ACGGTTTTGC
401     TTGCCGACCC GTCGCCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451     GAGGCTTGCC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501     CGTGCCGAAA AAAGCGGAGG CGATTTCAA TAAATTGTTT TTCACACATC
551     ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```


601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)
 1 ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
 51 LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
 101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
 151 EAWQTREGNL AGKILAVVVK KAEAISNKL FTHHPKRQTE FAVGQVKKWR
 201 AY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG CGCGCGGGA TTTCATATTT
 151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
 201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251 AGCTGGATAA GGAGCAGATG CGCGCGTCTG TTGAGGATAT GCGGCGCATT
 301 ATGCCTGATT TGGGTTTTGA GGCGAAGGCG TATGCCCTGT CTTTCGAGCA
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
 451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGGA
 501 TGCTTGCGAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601 CCAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCAGTGC
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep
 1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
 101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

		10	20	30	40
g952.pep		LSYRLNAAPMFNDNPVYVGKIKLQSWKARRDFNIVKQDLDSCG			
m952		MMKFYVFLACVVVLSYRLNAAPMFNDNPVYVGKIKVQSWKARRDFNIVKQDLDSCG			
	10	20	30	40	50
	50	60	70	80	90
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGF EAKGYALSFEQLAQ				
m952	AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGF EAKGYALSFEQLAQ				
	70	80	90	100	110
	110	120	130	140	150
g952.pep	LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTREGNLAGKI				
m952	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI				
	130	140	150	160	170
	170	180	190	200	
g952.pep	LAVVPKKA E A I S N K L F F T H P K R Q T E F A V G Q V K W W R A Y X				
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE				
	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

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```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATT TTTCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTGC
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VTKKLDKEOM RASFEDMRRI
101 MPDLGFCAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

a952.pep	10	20	30	40	50	60
m952	10	20	30	40	50	60
a952.pep	70	80	90	100	110	120
m952	70	80	90	100	110	120
a952.pep	130	140	150	160	170	180
m952	130	140	150	160	170	180
a952.pep	190	200	210	219		
m952	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGCAGAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCCCTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTCCACCA AATTCAACTT CAACGGGAAA AAACCTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACGCCCCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGACCAAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

```

g953.pep
1  MKKIIFAALA AAAGVTASAT YKVDEYHANV RFAIDHENTS TNVGGFYGLT
51  GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF
101 VSTKFNFNKG KLVSV DGNLT MRGKTAPVKL KA EKFN CYQS PMAETEVC GG
151 DFSTTIDRTK WGV DYL VNAG MTKNVRIDIQ IEAAKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

```

m953.seq
1  ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
51  CTCGCCGCCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTCAACACC AGCACCACCG TCGCGGTTT TTACGGTCTG
151 ACCGGTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCGTCAAA CTCAAAGCCG
401 AAAAAATCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

```

m953.pep
1  MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNFNK KLVSV DGNLT TMHGKTAPVK LKA EKFN CYQ SPMEKTEVC G
151 GDFSTTIDRT KWM DYL VNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

	10	20	30	40	50	60
m953.pep	MKKIIFAALAAAISTASAA TYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
g953	MKKIIFAALAAAAGVTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	
	70	80	90	100	110	120
m953.pep	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL					
g953	RDGKIDITIPVANLQSGSQPF TGHLSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m953.pep	TMHGKTAPVKLKA EKFN CYQSPMEKTEVCGGDFSTTIDRTKWM DYL VNVGMTKSVRIDI					
g953	TMRGKTAPVKLKA EKFN CYQSPMAETEVC G GDFSTTIDRTKWM DYL VNAGMTKNVRIDI					
	120	130	140	150	160	170
m953.pep	QIEAAKQX					
g953	QIEAAKQX					
	180					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

```

a953.seq
1  ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
51  CTCGCCGCCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
101 CTATCGACCA TTCAACACC AGCACCACCG TCGCGGTTT TTACGGTCTG
151 ACCGGTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAACC TGCAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAACTGG TTTCCGTTGA

```

1366

```

351 CCGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNI TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAAIGTASAA	TYKVDEYHANARFSIDHFNT	STNVGGFYGLTGSVEFDQAK			
m953	MKKIIIFAALAAAAISTASAA	TYKVDEYHANARFAIDHFNT	STNVGGFYGLTGSVEFDQAK			
	10	20	30	40	50	60
a953.pep	RDGKIDITIPVANLQSGSQH	FTDHLKSADIFDAAQYPDIR	FVSTKFNENGKKLVSVDGNI			
m953	RDGKIDITIPIANLQSGSQH	FTDHLKSADIFDAAQYPDIR	FVSTKFNENGKKLVSVDGNI			
	70	80	90	100	110	120
a953.pep	TMHGKTAPVKLKAKEFNCYQ	SPMLKTEVCGGDFSTTIDRT	KWGM DYLVNVGMTKSVRIDI			
m953	TMHGKTAPVKLKAKEFNCYQ	SPMEKTEVCGGDFSTTIDRT	KWGM DYLVNVGMTKSVRIDI			
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAAACAGG CCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAATCA ATGCAAGAAT GCCGTAAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDL D KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGatgaag gcgaacagtc tttggttcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaagtgtc gaattattt tgaataacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggtatggc taacgycgga
951 tatgcaaac tatcatgcgc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKKAQKWFH VTEQEHGEEV WLDYIIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MREIMPRGMK ANSLVVGYDA DGLPQKVYWS VDNKKPKQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGTTGCGG
401 TTTTCGCTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGA
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAG
701 AGAGCAACCG AATTGCGTGC GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTGCACAATG
851 GAAAAAACC CGAGAGTTTC GAATATTATT TGAATAACGG AAATCTTTT
901 ATTGCACAA CTTCGACGCT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGCGGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKKAQKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFNA					
	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
g957.pep	310	320	330			
	IAQSSTVTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTGTG	CACTTGATTT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTGTAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTGTG	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATCAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCCG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGAATCGCGC	GATTCTGTGT	TTTATCAGAA	TATCGGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

```

951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGCGCG GACCTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MEKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCGYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA				
m957	10	20	30	40	50
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA				
a957.pep	60	70	80	90	100
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLAALAVRLSRLKEKAKWFHVTEQEHGEEV				
m957	60	70	80	90	100
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLAALAVRLSRLKEKAKWFHVTEQEHGKEV				
a957.pep	120	130	140	150	160
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
m957	120	130	140	150	160
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV				
a957.pep	180	190	200	210	220
	WQPDGVSVDASGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS				
m957	180	190	200	210	220
	WQPDGVSVDAAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS				
a957.pep	240	250	260	270	280
	DSRDSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF				
m957	240	250	260	270	280
	DSRNSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF				
a957.pep	300	310	320	330	340
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR				
m957	300	310	320	330	340
	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR				
a957.pep	360	370			
	YAEAAARRSGGRRDLSHX				
m957	360	370			
	YAEAAARRSGGRRDLSHX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCACG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGGCGGACG

```

```

101 GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCCTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCTA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCTCTAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTCTGGGGC
451 GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAAG GTCAGCCGCA
551 CCGCCGAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCCAATTC
601 AACACCTGTT CCGCCGAGAG TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTTCCGGCG CGTTCCCTTT TTCTATACGC CTTGGGCGGA CTTCCTCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCCGCCCC GGCATTATCG GCGAACCGCG CGCGACGTTT
901 GACGGCAACC TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCAG GCGGGCGGGA GGCAGCCTGA ATGCCGGCCT TTCGTTTCAG
1201 AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTACAGCA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGGCGG AAGCATCCG CGACGCTCGG GCGCGTTTTG
1501 CCGTGTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCCTG TTCTACAAC
1601 ATATTCTTGC CAAATCTCAA AACGACCTGC CCAATTTTCA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTTCTAT TCAAGGATGA TCGGTTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCG ACTGGGTGGC ATTCGCTCCG GCGGGCATAG
1901 GCGGGCGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCTTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAAC
2151 CGGTTTGAAG GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGCGGAAA ACACCTACAA AAACGCCGTC TTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1 LARLFSLKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51 SDLTLLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DVTVTGDRFA LQQDGTLLRG
151 ETLLTYNLDDQ TGEAHNVNME TEQGGRRLLQ VSRTEMLGE GRYKLTETQF
201 NTCASGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRLPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLRNRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLSDFGG KASRSVGRVL
501 PVVNIDGGTT FERNTRLFGG GVVQTIEPRL FYNYPKASQ NDLPNFDSSSE
551 SSFGYQGLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSPGKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDQDGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLLQLKDL S SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.seq
1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTG
51 CTTCCGCGAC CATTCGCGCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGGTCCGA ACCCATACAG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGAGCAT
251 CCATCCCCGA AGACTATACG CGCATGTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTCG AACGCAACCG
351 GACGACCCCT AATACCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTTCGG
451 GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGCRATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTGGGCG GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCCTC
651 TGTCCAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCTGCTT GTTCCTCAC TGTCCGCCGG
801 TTCGACCGCG GTTCCCTTT CCGTCCCTA TTATTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCGCG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGCG AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTACGG
1101 CAACAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GGGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCA CAATTTACCC GATTACGCGA CGACAGCCGC
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCC GACATCAAAT GGGATTTTCA
1401 CAACAGCTGG GGCTATGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACCGCT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAACCTT CGAGCCGCGC CTGTTCTACA
1601 ACTATATPCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGTC
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATCTT ATTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTGGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGCGCGG CCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCGCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGTA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

```

1 LARLFLSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PLSLSLSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVERNRRTL NTDWADYDQS GDTVTAGDRF ALQQDGTILR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLL SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPYFYN LAPNLDTFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWOHR HDISDTLQAG
351 VDENQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDLSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKEYFKDDAV MLDGVSQKPK RNRSDWVAFS SGSIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLG GAKEYSSCGC WGAGVVAQRY
751 VTGENTYKNA VFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

m958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
g958	LARLFSLKPLVLALGFCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC					
	10	20	30	40	50	
m958.pep	70	80	90	100	110	120
	LFCESNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
g958	LFCESNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
m958.pep	130	140	150	160	170	180
	NTDWADYDQSGDVTVTAGDRFALQQDGTILIRGETLTYNLEQQTGEAHNVNRMEIEQGGRRRLQ					
g958	NTDWADYDQSGDVTVTGDRFALQQDGTILIRGETLTYNLDQQTGEAHNVRMETEQGGRRRLQ					
	120	130	140	150	160	170
m958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKIGIVAKHAAAFVFGGVP					
g958	SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGIVAKHAAAFVFGGVP					
	180	190	200	210	220	230
m958.pep	250	260	270	280	290	300
	IFYTPWADFPDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLPNLDATFAPSVIGERGAV					
g958	IFYTPWADFPDGNRKSGLLVPSVSAGSDGVSLSVPYYFNLPNFDATFAPGIIGERGAT					
	240	250	260	270	280	290
m958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	300	310	320	330	340	350
m958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
m958.pep	430	440	450	460	470	480
	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNWSGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDGRQDGSRLVVYPGIKWDFSNWSGYVRPKLGLH					
	420	430	440	450	460	470
m958.pep	490	500	510	520	530	540
	ATYYSLNRFSGQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLERLFFNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIEPRLFFNYIPAKS					
	480	490	500	510	520	530
m958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLSAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
m958.pep	610	620	630	640	650	660
	QKFFYKDDAVMLDGSVGGKPNRSDWVAFASGSGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFFYKDDAVMLDGSVGGKPNRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
m958.pep	670	680	690	700	710	720
	SYRPAQGVKNARYKYGRNEKIYKSDGSYFYDKLSQLDLQAQWPLTRNL SAVVRYNYGF					
g958	GYRPAQGVKNARYKYGRNEKIYQADGSYFYDKLSQLDLQAQWPLTRNL SAVVRYNYGF					
	660	670	680	690	700	710

1373

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              730      740      750      760      770      780
m958 . pep    EAKKPIEVLAGEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||
g958          EAKKPIEVLAGEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958 . pep    MDVAVPGYITAHSLSAGRNRKP
              |||
g958          MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958 . seq
1  TTGGCTCGTT TATTTCCTACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTGCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGCCGA ACCCATAACG
151 CCTACCAAGC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCTG
451 GGCAGAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGCGATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTTCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCGCCGG
801 TTCGGACGGC GTTCCCTTT CCGTCCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCGCG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGCGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGTACAAAG ACAAACCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCGCC CAAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCGCAGCGCT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGTC
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAGACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCTG
1851 CAAAAAACCG CGCAGCGGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCAATAACA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGTACCGTCC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTTCGCG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958 . pep
1  LARLFLSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLSTGSL LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKIGIVAK HAAFFVFGGVP IFYTPWADFP

```

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251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLRN VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QTFRSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFG SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYLSKSGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRNYGF EAKKPIEVL GAELYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
a958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL					
m958	LFCSNESGSPERTEAAVQGSSEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL					
a958.pep	130	140	150	160	170	180
	NADWADYDQSGDVTAGDRFALQQDGTLLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ					
m958	NTDWADYDQSGDVTAGDRFALQQDGTLLIRGETLTYNLEQQTGEAHNVMEIEQGGRRLQ					
a958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP					
m958	SVSRTAEMLGEGHYKLTETQFNCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP					
a958.pep	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPPYFNLAAPNLDTFAPGVIGERGAV					
m958	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPPYFNLAAPNLDTFAPGVIGERGAV					
a958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDHDKKSGRNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTWLPDHDKKSGRNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
a958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLRNRRVWLDYGGRAAGGSNLAGLSVLKYQTLANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLRNRRVWLDYGGRAAGGSNLAGLSVLKYQTLANQSGYKDKPYALM					
a958.pep	430	440	450	460	470	480
	PRLSADWRKNTGTRAQIGVSAQTFRSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
m958	PRLSVEWRKNTGTRAQIGVSAQTFRSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
a958.pep	490	500	510	520	530	540
	ATYYSLNRFGSQEARRVSRTLPPIVNIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS					
m958	ATYYSLNRFGSQEARRVSRTLPPIVNIDSGATFERNTRMFGGEVLQLEPRLFYNYIPAKS					

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	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSESSFGYQQLFRENLYYGNDRIANTANSLAASVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSESSFGYQQLFRENLYYGNDRIANTANSLAASVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVMDGSGVGGKPRSRSDWVAFASGSGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKDDAVMDGSGVGGKPRNRSDWVAFASGSGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKP					
m958	MDVAVPGYITAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

```

g959.seq
1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

```

g959.pep
1  MNIKHLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAARAR VGKKTIDIL EHDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

```

m959.seq
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

```

m959.pep
1  MNIKHLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGKKTIDIL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DHGHAHQHNKQDKIISRAQAEKAALAR
g959	MNIKHL	LLTAAAT	LLGISAP	ALAHHD	GHGDD	DHGHAHQHNKQDKIISRAQAEKAALAR
	10	20	30	40	50	60

	70	80	90	100	109
m959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEYKVVVDARTGRVISSRRDDX
g959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEYKVVVDARTGRVISSRRDDX
	70	80	90	100	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLTAA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRLL	LTAAAT	ALMGISA	PALAHHD	GHGDD	DHGHAHQHSKQDKIISRAQAEKAALAR
m959	MNIKHL	LLTSAAT	LLSISAP	ALAHHD	GHGDD	DHGHAHQHNKQDKIISRAQAEKAALAR
	10	20	30	40	50	60

	70	80	90	100	109
a959.pep	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEYKVVVDARTGRVISSRRDDX
m959	VGGKIT	DIDLEH	DNGRPH	YDVEIV	KNGQEYKVVVDARTGRVISSRRDDX
	70	80	90	100	

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCC TTGTTTGAAG CTCCGCGGCT CCTGCCGAGC TTCACCGACC
101 CCGTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAACCAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCCGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGTTGTAG CGCGGCAAC GGCAGGCGTA TCCAACAAAC

```

```

551 TCGGTGCCTC TTCCCTTGCC ACTTGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTGA ACCTGGCCAA TCGGGGCGAG GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAATAA TGCGGTAAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTAGCCGAC AACCTGACCA CCTTATTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLLPS FTDPVVPKLS APGGYIVDIP
51  KGNLKTEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLNAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEASIKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNITDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLTFDETL
401 DWNDAKAVID IIVGTENLRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGRFYLDGQ
501 HKNHLEVFDK NGNFKFVLNM DGSINQMKTG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGA AGAGACTAAG ACAAAATATG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCGGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAACA
651 AAACGTGCGT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCTGTTCCT AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGCCTCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFPKLV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

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1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAGGY KESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet

a961.pep not found yet

g972.seq not found yet

g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

m972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCCGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAAATGGG TAAGGTTTCA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

m972.pep

```

1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FPDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDY YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

a972.seq

```

1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAGGTAC TGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCCTTGTTAG
551 ATCACGATAA TGTTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTGATCAG AGAAAGAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACCTG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCCGGGAT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACCTGATG AATTGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAA AGGCTTTTTC GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTIRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLVNFMIE MFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPTYDVE
401 KERKQYQYLS KVVHQNVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
a972	LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVS GCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
a972	DTLLKVS GCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTIRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTIRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFN YGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKTLNLTFE					
a972	SKWVRFEIQFN YGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKTLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972 . pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972 . pep	HEQPDIDLEIELDELGVIAFKNSDKFEDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFEDREKRLFSPTYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420

m972 . pep	YFX
a972	YFX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973 . seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCC
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCCA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CTGCGCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgteggg gacatCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCAATC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcaagaagc cgacaccatc ggcggctTGG
701 TCATTACAGA ATTGGGACAC CTGCCCGTGC GCGCGGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcacgct CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973 . pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLROAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVLII
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973 . seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCC
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCGGCAGC GAATACAGCA kCGAAGAAGC CGACACCATT GCGGCGCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
 751 GCGCGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG BIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
g973	EQFHLKSVLRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	BIEDEFDEDD SADNIHAVSS ERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYGSSEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCGTCAT CGGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAAC TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GCGGCGCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGGCTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVILGILHA KDLLKYMFPN EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIEEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFPN					
a973	RDAMITRSRMNVLKENDSIE RITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFPN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIEEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIEEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATR.VKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATR.VKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTCAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTCTTG AACCAACGGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCTGAT TATCAAAGAA CTGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAAACAAAC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```

g981.pep
  1  MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101  GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK NMNKVGVTG
151  HTGDFSUSKL LGNDNPFIAR FENVPLIIEK LENGGLDSVV SDSAVIANV
201  KNNPAKGMDF VTLPDFTTEH YGIAVRKGD EATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE GQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```

m981.seq
  1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
 51  TGCCTGCGGC GGTGAGGGCA AAGATACCGC CGCGCTGCC GCCAACCCCG
101  ACAAGTGTGA CCGCGTGGCT TCCAACCGCG AGTTTGCCCC CTTTGAATCT
151  TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201  GATGGCGAAG GCGGGCAATT TTAATATCGA ATTCAAACAC CAGCCGTGGG
251  ACAGCCTTTT CCCGCGCTTA AACACGGCG ATGCGGACGT TGTGATGTCG
301  GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351  GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401  CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451  TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAATCCGAA
501  AATCGCGCGC TTGAAAAACG TTCCCTGAT TATCAAAGAA CTGGAACG
551  GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
601  AAAACAAATC CCGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651  CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701  AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751  AAGATTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801  A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```

m981.pep
  1  MKKWIAAALA CSALALSACG GQKDAAPA ANPDKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101  GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK NMNKVGVTG
151  YTGDFSUSKL LGNDNPFIAR FENVPLIIEK LENGGLDSVV SDSAVIANV
201  KNNPAKGMDF VTLPDFTTEH YGIAVRKGD EATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE DGAAK*

```

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKWIAAALACSALALSACGGQKDAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
g981	MKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGKKVSSSEDLKNNMKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIEK					
g981	ITQVVLVPGKKVSSSEDLKNNMKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIEK					
	130	140	150	160	170	180
981.pep	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGD EATVKMLNDAL					
g981	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGD EATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACCAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCGTGGTTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801  A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQGKDAAPAA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVTG
151 YTGDFSVS KL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAPAAANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPKGKVSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGKVSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVSDSAVIANVKNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVSDSAVIANVKNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcacgcg aaaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatatatttgc cggccgcCga ttgggtagcC ttgGGcgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAACgagCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAGgca TGAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGcgg ttgCCGCTtt ggttgAAGAg cTGA AAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGCG AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTTCG AAAAAAAAT CAGCAACATC CGCGACCTGC
701 TCGCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTTccGAAG Aagtcggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTATcG
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAGAAA AACTGCAAGA
1101 CGCGCTTGCC AACTTGCGAG GAGGCGTGGC AGTGATCAA GTCCGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTAtc GCCGGTCTGA TGCTGACGAC
1551 CGATGCGATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGAAT GGGCGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRGI DKAAALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLNELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTTGGV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGVALL RARAALNLH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKNGYGYNA GSGEYDMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA AAGACGTACA GTTCGCAAT GAAGTCGTC AAAAAATGTT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGCG AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAA CAAATCGCTG CTTTGACAA

```

651	TCCGTTTGTA	TTGTTGTTCC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAAGT	GCAAAAGCCA	GCCGTGCGCT	GTGATTATC
751	GCTGAAGACG	TAGAAGGCCA	AGCCTTGCGC	ACTTTGGTGC	TGAACAACAT
801	CCGAGGCATC	CTGAAACCG	TTGCCGTCAA	AGCCCCGTGC	TTCCGCGACC
851	CGCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCTGTACCGG	CTGCGCTGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTTG	CGACGCAGCC	CAAATCGAAG	CGCTGTGTCG	CGAAATCCGC
1051	CAACAATATG	AAACGCGAAC	CAGCGATTAC	GACAAGAGAA	AACTGCAAGA
1101	CGCGTGGCT	AAATTGGCAG	CGCGCTGGCG	AGTCATCAA	GTCGGTGGCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAAGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCCGT	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGAGGCGGTA	CAATCGTCT	TGCGCCCGGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGCT	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGTCAT	ATCGCTGAAA	TCCCCGAAGA	CAAACGGGCT	GTGCCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GQCGGCATGA	TGTA	

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGCAAT	GAAGTCCGTC	AAAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCGGT	CCGCGTAACC	TTGGGCCCCA
101	AAGGTCGCAA	CTAGTCTGTT	GACCCGCGAT	TCGGCGGCCC	GCACATCACC
151	AAAGACGGCG	TGAACGCTCG	CAAGAAAGAT	GAACTGAAGG	ACAAGTTTGA
201	AAATATGGGC	CGCGAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGCGA	CGGTACGACT	ACCGCACCCG	TACTGGCGGA	ATCCATCGTT
301	GCCGAAGGTA	TGAATATATG	TACCCGAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	GATAAAGCCG	TCGCGCGTTT	GTTTGACGAA	CTGAAAACAA
401	TCGCCAAACC	TTGCGACACT	TCTAAAGAAA	TCGCCCAAGT	CGGCTCTATT
451	TCCGCCAACT	CCGACGAACA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGTCGCG	AAAGAAGGCG	TGATTACCGT	TGAAGACCGG	AAGTCTTTGG
551	AAAACGAGCT	GGACGTAGTT	GAAAGTATGT	AGCTTCGACG	CGGCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAA	CAAAATCGTG	CTTTGGACAA
651	TCCGTTTGTA	TTGTTGTTTC	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCTCTGTTT	GGAACAAGTG	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAACCCG	TTGCCGTCAA	AGCCCTGGC	TTGGCGGACC
851	GCCGCAAAGC	GATGTGTCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AGTTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGATCT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCC	CAAAATCGAAG	CGCGTGTGCG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGCGTGGCG	AGCTCATAAA	GTCGGTGGCC
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	AGCCGCTGGA	AGACGCGCTG
1201	CACGCTACCC	CGCGACCCGT	TGAAGAAGGC	GTGGTTGCAG	CGGGCGGCGT
1251	AGCCCTGTGT	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAAATCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGCAAAA	CTGTTGCCAA	CGCAGGCGGC	GACCCGACG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAAG	GCAACTACGG	TTACAACGGC	GCGACGGGGG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCAT	TGCAACAACG	CGCATCTATC	GCCGCGTTGA	TGCTGACCAC
1551	TGATTTCATG	ATCGCTGAAA	TCCCCGAAGA	CAAAACGGCT	GTGCTCTGTA
1601	TGGCGCGCAT	GGGTGGTATG	GCCGCGCATG	TGTAA	

m982/g982 95.8% identity in 544 aa overlap

10 20 30 40 50 60
 m982.pep MAAKDVFQGNVEVRQKVMNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
 : ::::: | : ||||| | | : || ||||| ||||| ||||| ||||| ||||| |||||

1387

g982	IASQNLRFDNRFLOKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
	70 80 90 100 110 120
m982.pep	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPTDLKRG
g982	ELKDKFENMGAQMVEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPTDLKRG
	70 80 90 100 110 120
	130 140 150 160 170 180
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
	190 200 210 220 230 240
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
	250 260 270 280 290 300
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
	310 320 330 340 350 360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDFGDAAQIEARVAEIRQQIETATSDY
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
	370 380 390 400 410 420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVGAGG
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVGAGG
	370 380 390 400 410 420
	430 440 450 460 470 480
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLGKNGYGYNA
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNKVLGKNGYGYNA
	430 440 450 460 470 480
	490 500 510 520 530 540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
g982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

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401 TCGCCAAACC TTGCACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGACAA
651 TCCGTTTGTG TTGCTGTTTCG ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAAACCC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 CGCGGTGGCC AAAGTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGGCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGTGTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CCGCCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGC GCGCGCTG TAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGTTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCGCG CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CCGCTCTATC GCCGCGCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
  1 MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
 51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDV V EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV L LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI L KTVAVKAPG FGDRRKAMLQ DIAILTGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

```

m982/a982 99.3% identity in 544 aa overlap

```

              10      20      30      40      50      60
m982.pep      MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              |||
a982           MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              10      20      30      40      50      60

              70      80      90      100     110     120
m982.pep      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIIVAEQMKYVTAGMNPTDLKRG I
              |||
a982           ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIIVAEQMKYVTAGMNPTDLKRG I
              70      80      90      100     110     120

              130     140     150     160     170     180
m982.pep      DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
              |||
a982           DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m982.pep      KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
              |||
a982           KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
              190     200     210     220     230     240

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	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGTV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

```

1  GTGTTCAAAA AATACCAATA CTTGCTTTG GCGGCACTGT GTGCCGCCTT
51  GCTGGCAGGC TCGGAAAAGG CAGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGTGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAA
401 ACGGCTACAT CTTGACCAAT ACCCAGCTCG TTGCCGGTAT GGCAGATATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TACCCGTCGT CAAAATCGGC AATCCCAAAA ATTTGAAACC GGCAGATGG
601 GTCGCTGCCA TCGGCGCGCC CTTGCGCTTT GACAACAGCG TGACCGCCGG
651 CATCGTGTCG GCCAAAGGCA GAAGCCTGCC CAACGAAAGc tACACACCCT
701 TCATCCAAAC CGACGTGTCG ATCAATCCGG GCAATTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGt cgTCGGCATC AATTCGCAA TATACAGCCG
801 CAGCGgcgga ttCATGGGCA TCTCCTTTGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAGGA AGTATCCTAC GGTTCGGCAC AGTCGTTCCG
951 TCTGGATAAA GCCAGCGGCG CATTGATTGC CAAAATCCTT CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGCGGGGCG ACATCGTCTT CAGCCTCGAC
1051 GCGGAGAGAA TACGTTCTTC CGGCGACCTT CCCGTCATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA
1151 TCACAATCAA AGCCAAGCTG GGCAACGCCg ccgagcATAC CGCGcatCA
1201 TCCAAAAACAG ATGAAgcccc ctacaccgAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGca
1301 aacacctcgt cgtcgtacgg gtttccgacg cggcagaacg cGCAGGCTTA

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1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPM PEIPQEEADD GGLNFGSGFI ISKNGYILT THVVAGMGS
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGFL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQ L KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTCTAC
 301 GAATTTTCA AACGCCTCGT CCGAATATG CCCGAAATCC CCCAAGAAGA
 351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCAGTCG TTACCGGCAT GGGCAGTATC
 451 AAAGTCTGCT TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCCGCCA TCGGCGCGCC CTTGCGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGCGATC AACTCGCAAA TATACAGCCG
 801 CAGCGGCGGA TTCATGGGCA TTTCTTCGCG CATCCCGATT GACGTGCGCA
 851 TGAATGTCGC CGAACAGCTG AAAAAACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
 951 TTTGGACAAA GCCGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
 1001 CCGCAGAACG TGCCGCGCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
 1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
 1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA
 1151 TCACCAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
 1251 GGTGCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
 1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
 101 EFFKRLVPM PEIPQEEADD GGLNFGSGFI ISKNGYILT THVVTGMGS
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGFL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQ L KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	:	:				
g986	VFKKYQYFALALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	GGLNFGSGFIISKNGYILTNTHVVGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
g986	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACCGCAGCA
251 GCAATGCCGA AACCATTCC GACCCGCTTG CCGACAGCGA CCCGTCTTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCTG TTACCGGCAT GGGCAGTATC
451 AAAGTCTGCT TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCCGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TACATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCTTTCG CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGCGCG CACTGATTGC CAAAATCCTG CCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTGGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPEEADD GGLNFGSGFI ISKDGYYLTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTQVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO

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1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQHTD SSGGHLVVVR VSDAERAGL
 451 RRGDEILAVG QVPVND EAGF RKAMDKAGN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
m986.pep	VQSEGPAVVNIQAAPARTQNGSGNAENDSDPIADNPFYEFFKRLVPMPEIQEEADD					
a986	VQSEGPAVVNIQAAPARTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIQEEADD					
	70	80	90	100	110	120
m986.pep	VQSEGPAVVNIQAAPARTQNGSGNAENDSDPIADNPFYEFFKRLVPMPEIQEEADD					
a986	VQSEGPAVVNIQAAPARTQNGSSNAETSDPLADSDPFYEFFKRLVPMPEIQEEADD					
	70	80	90	100	110	120
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA					
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA					
	190	200	210	220	230	240
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
a986	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
a986	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
	430	440	450	460	470	480
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG

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51  TTCTTCATGG TTGCCCCCAG TGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTT
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GGCATCCCAA TactaagtG CGCCTGTTCA ACCCCTtctg CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTPSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDDLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSIFYVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAANKLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAG TGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GGCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCGG TTCGCGCGGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
  1 MKTRSLISLL CLLLCS CSSW LPPLERTES RHFNTSKPVR LDNILQIRHT
 51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERGV VRVRLLEDN NTRGLD LLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDIVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHD PATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCS CSSWLPPLERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCS CSSWLPPLERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVVRVRLLEDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNMYLAERGVVRVRLLEDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLD LLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLD LLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDIVTVLTNSLQATDVA					

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g987      |||||
          RKPP|IAGRLQDALKQPEKSV|LVSPYFVPTKSGT|DALAKLVQDGIDVT|VLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          |||||
g987      AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNR|LQWHPATRK
          |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNR|LQWHPATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTGGAACG ACCCCACGCA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTC AACCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 TCTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TTCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCTT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCGGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCGCGACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFN|TSKPVR LDN|ILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLD|LQYYIW RND|ISGRLLF
101 NLVYLA|AERG VRVRL|LLDDN NTRGL|DDLLL ALD|SHPNIEV RLF|NPFLVRK
151 WRALGY|LTDF PRLNR|RMHMK SFTAD|NRATI LGGR|NIGDEY FKV|GEDTVFA
201 DLDILA|TGSV VGEVS|HDFDR YWASH|SAHNA TRI|RSNGIG KGL|QALGYND
251 ETSRHA|LLRY RETVE|QSPLY QKIQT|GRIDW QSVQ|TRLISD DPA|KGLDRDR
301 RKPP|IAGRLQ DALKQ|PEKSV YLVSP|YFVPT KSGT|DALAKL VQD|GIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAANKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLP	PLEERTESRHFN	TSKPVRLDNILQIRHT	PHTNGLSDIY		
a987	MKTRSLISLLCLLLCSCSSWLP	PLEERTESRHFN	TSKPVRLDNILQIRHT	PHTNGLSDIY		
	10	20	30	40	50	60
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA	LAERGVRVRL	LLDDN			
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLA	LAERGVRVRL	LLDDN			
	70	80	90	100	110	120
m987.pep	NTRGLDDLLALD	SHPNIEVRLFNP	FLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI			
a987	NTRGLDDLLALD	SHPNIEVRLFNP	FLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI			
	130	140	150	160	170	180
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL	TNSLQATDVA				
a987	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL	TNSLQATDVA				
	310	320	330	340	350	360
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR	LQWHPATRK				
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR	LQWHPATRK				
	430	440	450	460	470	480
m987.pep	TYPNEPEAKLWKRIAANKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIAANKILSLLPIESLLX					
	490	500	509			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq
 1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTGTG TCAAATGccg Cgtcggaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTTCGTT TTATACGAAC GCCAgatgcg tggTgcatG CAcggcgaca
401 ccgttACCGT CCGTCTGCG ggtatggaCC GCAGGGGccg ccgcGAAggg
451 acgtttctGG ATATTGTGCA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTTGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGgaaAAAA ATtcccagacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCTT TTGGTAACGA
851 TAGACGCGGA AAGCGCGCG GATTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGCGGA ATGTTTGC CGCGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCGGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCAT CCGCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGAAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCTGTGAA ATATTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCGGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAGGGGAA ATCGAAAAAC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGCGGT
2301 GCCTGCCGTT GCCGAATCGG GAAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHLPLS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFVAF LMPMDEGDFV LYERQMRGVM HGDVTVTRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFFDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMYRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRENMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKKRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```

m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TGCAGAAAAA ATCCCGTCC ATGTACGCAA
351 AAGCGATTG AAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCG GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTG
501 TGTCGCCCTT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT GTCGCTCAA TCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAAA
751 TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCTT
801 TTACAAATC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGC GCAGGATTTC CTGTTGAAAA
1001 ACAAGCATA GGCCTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATA GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATTT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC

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1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLPHQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGD	TVTVRPA	GMDDRRGRREGT	FLDIVERAQSKVVGRFYMDRGVAILEPED		
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVY	PEQNRP	AVAKIIEVLGDYADSGMEIEIA		
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVY	PEQNRP	AVAKIIEVLGDYADSGMEIEIA		
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP	LVTIDGETARDFDDAVFAEK			
g988		VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDL	CDLPVTIDGETARDFDDAVFAEK			
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRR	VIPMLPENLSNGICSLNPDV			
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRR	MIPMLPENLSNGICSLNPDV			
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWK	WISDGIDHPYKAQIDTLYKL			
g988		ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWK	WISDGIGNPHKAQIDTLYKL			
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRN	DAHKLIEECMLAANVCAADF			
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRN	DAHKLIEECMLAANVCAADF			
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDN	PSPKDYAALVEQFKGRPDAE			
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDN	PSPKDYAALAEQFKGRPDAE			
	390					

1401

	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNRRKTYTP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTYMYMRDKVGEVFEGKIS-GMTSFGIFVTLD					
g988	NKSWQALGVHTSFCERRADDAGRDVENWLKTYMYMRDKVGEIFEGKISRGVANFGIFVTLD					
	610	620	630	640	650	660
m988.pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
m988.pep	570	580	590	600	610	629
	IAGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAEKKTARCKVRGVPVAESGKKAKKP					
	730	740	750	760	770	780
m988.pep	630	640				
	VPIKVKKRKGKXS					
g988	VPIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1   ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTGCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGGACAAA TTGGATTGGG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTG TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACGTG TCGTCCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCTG ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGA AATTGCC GTGCGCAAGC ATCATTGGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGGAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTGG AAAGGCCGCG TCGATTGGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTGCTGGCG ATTGCCGATG TCAGCCATTA
951 GTGCCGCCCG GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGACCCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTTCA GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTCAAATCTT TTCAAATCC TTCAGAAAAA GCGTTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCGGT GTGCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCTT TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1402

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1701 CGAAGCATAAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAAATCTC CGGCATGACC
1951 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATTT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pep
1  MNKNIKSLNL REKDPFLSRE KQRYEHLPLS REWIIELLER KGVPSKIEAL
51  VRELSIKEEE YEFFERLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
101 HKDRFGFAVP LTPAKDGDFV LYERQMRGIM HGDIIVTRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGRFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SQQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAKK IPDHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPRR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
601 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA
751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

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m988/a988 97.0% identity in 641 aa overlap

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                                10      20      30
m988.pep                                TVLDIVERAQSKVVGRFYMDRGVAILEPED
                                |||
a988      LYERQMRGIMHGDIIVTRPAGMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED
                                130      140      150      160      170      180

                                40      50      60      70      80      90
m988.pep      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                |||
a988      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
                                190      200      210      220      230      240

                                100      110      120      130      140      150
m988.pep      VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                |||
a988      VRKHHLPHQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK
                                250      260      270      280      290      300

                                160      170      180      190      200      210
m988.pep      VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a988      IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV
                                310      320      330      340      350      360

                                220      230      240      250      260      270
m988.pep      ERLCMVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGDIDHPYKAQIDTLYKL
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a988      ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

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1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
m988.pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
m988.pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
m988.pep	460	470	480	490	500	510
	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
m988.pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
m988.pep	580	590	600	610	620	630
	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTAGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTAGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
m988.pep	640					
	PIKVKKRKGKSX					
a988	PIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCCAGCA	TTCAATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTCTAATAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCGT	GTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTGCAAC	CTGTGCGCGC	GTGGAACCTC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAA	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	GA AAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAATG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCGGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGACAGCAA AGGTGCGTCT TCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

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-- This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
  1 MTPFTLKKTIV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
 51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAQAQIKAD GHADVKGSDW GVGQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSKADLFGD VTWTRHSREN KAELEFEKEK NIANGKSDR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
  1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGTC AACGCCAACA TCGTGTGCGC CAGCATTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCGAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCGCGGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TCGGCAATA TGCCGACTGG GGGATTAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACTAA CCGTGTAGCC GAAGCTCAA AAATTGAGG
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAATTAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGC
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTA AAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCATATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
  1 MTPSALKKTIV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
 51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKFPKPNGVA EAAKIQADGH ADVKGSWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAWEAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNHRHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSAEILTAKPPKNGVAEAAKIADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGADEWAADGAAKQWQNDNMLTPLYTANERKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGADEWAADGAAKAMWS-TMLAANGYTANERKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMKVSDKADLFQDVTWTRHSRFEKAEKNIANGKKSDDRTTITPNWRNTYK				
m989	LSVHGMKVSDKADLFQDVTWTRHSRFDKAEKLVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	350	360	370	380	390
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGLGGSYQISEPLQLRVGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	410	420	430	440	450
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAACCGTC TACTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTCCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCAGCGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
 201 GATTTCGCTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCCGGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TCGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGG
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATCGCGAA TGGGCGGCGAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTC GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTCTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCCG
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```
a989.pep
  1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
 51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGD AE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLEGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAA YTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKEK*

m989/a989 93.1% identity in 467 aa overlap

      10      20      30      40      50      60
m989.pep MTPSALKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      MTPSALKKTVLLLGTAFAAAASQASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
      10      20      30      40      50      60

      70      80      90     100     110     120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
      70      80      90     100     110     120

      130     140     150     160     170     180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
      130     140     150     160     170     180

      190     200     210     220     230     240
m989.pep SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
      190     200     210     220     230

      250     260     270     280     290     299
m989.pep NDRARVGVNYRSKVSHTLKGD AEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      NDRARVGVNYRSKVSHTLKGD AEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES
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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAE	LVFEKEKTVVKGKSDRTTITPNWRNTYKV				
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAE	LVFEKEKTVVKGKSDRTTITPNWRNTYKV				
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTCTCTGTTT GGCTACGACG
701 TCGGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTTGGA ACGCCGCGCG GAAAATCTGA AAACGCTCGA
801 CCGGCGCAAA CTGATTGCGG CAAAAACGGC GGATTCCGGT TCGTTTTCGT
851 TTAAACAAAA TTACCGGCAG GGAATGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCGCA TCCGTCCTGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTCGCATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGCGTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCGC
1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGCT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELT MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVO IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKXIRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGT VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLFL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTCCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATAACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTTAAGAAG CAATTACAGG ATTTATACAA AACAAAGACC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGACCA AAATTTAGTA TACTCAAACA GAAAACCCC GATTAAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCTT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAATGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGC TGGTTTGGGA ACGCCGCGCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAATACT TTGTTGGGCG
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CCGGCTGATG
1201 GCGGCGAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTGAAGG CCGCTACAAC GCGCTTGTGG
1451 CGGAAGGCGT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCGG
1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGATTGT CCGTCAAATG
1851 GCTGTTTTGA

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This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKYITDITY GDNLDKAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELT MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVO IGGEVFVRQN EGSRLAIGVM

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WO 99/57280

1409

401 GGRAGQHASV NGKGGGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
 501 QAQFTYLGVN GGFTDSEGTA VGLLGGGQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAQRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRITDGDKE AALSLKWL*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	130	140	150	160	170	180
m990.pep	KFSTLKQTMFDLINKLVDSVLTSPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVDSVLTSPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	250	260	270	280	290	300
m990.pep	ALTFFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFFEEKVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFQKQNYRQGLYELLKQC					
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
a990	RSHQNIRGGAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
	430	440	450	460	470	480
m990.pep	LYGYGGGVYA AWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYA AWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTA VGLLGGGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTA VGLLGGGQWQSRAGIRAKTR					
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAQRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAQRTALEGRFGIEAGWKGHMSARIG					

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	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTGACGCGG  CCCGTTCCGC  GACGGGCATC
201 GCGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAGTTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGGT
701  AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDLNLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGGCGGGCAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GCGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCCTG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATTG
501 TAAAGTTTAT  GCTAAAGAAC  AGCAGGATAA  GGCGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701  AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDLNLQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

WO 99/57280

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```

      10      20      30      40      50      60
m992.pep  MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
g992      MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA
          |||||

      70      80      90      100     110     120
m992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||
g992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||

      130     140     150     160     170     180
m992.pep  LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||||
g992      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
          |||||

      190     200     210     220     230
m992.pep  ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX
          |||||
g992      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX
          |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```

a992.seq
1  ATG TTCAGAC GGCATCGGCA TTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCT TGTCGCTTTT GGGTGCGTTG GGTTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGCGCAG GGGACGCGGG TTCCGACGCG CCCGCCCGCC GCCGAGCATC
201 GCGCAATACC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTCGACAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTG
501 TAAAGTTAT  GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGGCGAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```

a992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGT VSKVYDGD TLHVIDGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFDTRY QREVAQVSVG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQAE ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWM DAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

```

      10      20      30      40      50      60
a992.pep  MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
m992      MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||

      70      80      90      100     110     120
a992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||
m992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||

      130     140     150     160     170     180

```

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```

a992.pep      LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
|||||
m992          LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIWX
|||||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDDAVGEWLGIWX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1      CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51     CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGGAAA
101    TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAGC CTATCAGTTT
151    GATTGGCGG CGGAATATCT TTTGATGGC GCAATGCTGA TTGAAATCAA
201    ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251    ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCTACGA GCAAATGAAA
301    CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351    GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGAG
401    TTTACATCGC CGATTGTATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451    AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501    GCAAATGACG GCAATCCTGC GCCGTTTGA GAAACACGGG ATATGCAGGT
551    TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601    TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651    GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701    ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1      LKVVLSFQG PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51     DLAAEYLLMA AMLIEIKSRL LLPRTAEVED EEADPRAELV RRLAYEQMK
101    LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151    KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201    FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1      TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51     TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCG ATGGTGAAGA
101    TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151    GATTGGCGG CGGAATATCT TTTGATGGC GCAATGCTGA TTGAAATCAA
201    ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251    ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301    CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGAGCCGAGC GGGATTTCGC
351    GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCAGAG
401    TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451    AAACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGCGCGC
501    GCAATGACG GCAATCCTGC GCCGTTTGA CGGACACGGA ATATGCAGGT
551    TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTCAAC
601    TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651    GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701    ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1      LKVVLSFQG PLDLLLYLIR KQIDVLDIP MKVITEQYLH YIAQIETYQF
51     DLAAEYLLMA AMLIEIKSRL LLPRTETVED EEADPRAELV RRLAYEQMK
101    LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151    KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201    FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

```

      10      20      30      40      50      60
m993.pep LKVVLSFGQGPLDLLLYLIRKQNIQVDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g993      LKVVLSFGQGPLDLLLYLIRKQNIQVDIPMVEITGQYLHYIAQMEAYQFDLAAEYLLMA
          10      20      30      40      50      60

      70      80      90      100     110     120
m993.pep AMLIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g993      AMLIEIKSRLLLPRTAEVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY
          70      80      90      100     110     120

      130     140     150     160     170     180
m993.pep LPLEIAVEAKLPEVYITDLTQAWLGILSRKHTRSHEVIKETISVRAQMTAILRRLNKG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g993      LPLEIAAETKLPEVYIADLMQAWLGILSRKHTRSHEVIQETLSVRAQMTAILRRLNKG
          130     140     150     160     170     180

      190     200     210     220     230     240
m993.pep ICRFHDLEFNPKQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g993      ICRFHALFNPEQGAAYVVVNFIALLELAKEGLVGIVQEDGFGEIRISLNHEGAHSDGIFG
          190     200     210     220     230     240

      249
m993.pep TRGGRDVF
          |||||
g993      TRGGRDVF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

```

a993.seq
1   CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGAAGA
101 TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCGCTG TGGCTTACGA GCAGATGAAG
301 CTGCGCGCAC AAGGGTTGGA TGCCTTCCT CGTCCGGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAATTGCCGT CGAAGCCAAG CTGCCCAGAG
401 TCTATATTAC CGACTTGACG CAGCGCTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAA GAAACCATCT CCGTGCGCGC
501 GCAAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
551 TTACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAT TGTGGAGCT TGCCAAAGAA GGTTTGGTCG GAATCGTACA
651 GGAAGTCGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGGGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

```

a993.pep
1   LKVVLSFGQ PLDLLLYLIR KQNIQVDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSR LLPRTEVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLEFN EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

```

      10      20      30      40      50      60
a993.pep LKVVLSFGQGPLDLLLYLIRKQNIQVDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m993      LKVVLSFGQGPLDLLLYLIRKQNIQVDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA

```

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGCGCGTTGC  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCCC
151 GGCGAATCCT  ACCCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TGCACAAAGT  TCCCGAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAATCATC  GAAACCGTGC  AAAAGGAAAA  CATCCCGGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACTG  GCGCGTTGT  TCGGGCATT  GAGCGACCAT
451 CCGCTGTATG  AGGATTGTG  CGAGGAATAC  GGCATTCCGT  TGTTCGCGCG
501 CCGCTGGGCG  GAAATTTTG  GCAATAATA  TCTGAAATCC  GACCAATATC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTC  CCGAAATTT  GAATCAATTT
601 TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGDTSQAAL  SRLPALLARK  PKLVIVGIGG
101 NDPLRKVPPE  QTRANIAKII  ETQKENIPA  VLVGVPHITL  GALFGLHSDH
151 PLYEDLSEY  GIPLFGGAWA  EILGNLNLKS  DQIHANGKGY  RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGCGCGTTGC  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCCCT
151 GGCGAATCCT  ACCCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TGCACAAAGT  TCCCAAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAATCATC  GAAACCGTGC  AGAAGGAAAA  CATCCCGGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACTG  GGTGCGTTGT  TCGGGCATT  GAGCGATCAT
451 CCGCTGTATG  AGGATTGTG  CGAGGAATAC  GGCATTCCGC  TGTTCGCGCG
501 CCGCTGGGCG  GAAATTTTG  GCGATAATA  TCTGAAATCC  GACCAATATC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTT  CCGAAGATT  GAATCAATTT
601 TTGAGAAAAC  AGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGDTSQAAL  SRLPALLARK  PKLVIVGIGG

```

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS DH
 151 PLYEDLSEY GIPLFGGAWA EILGDN NLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	70	80	90	100	110	120
	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGDN NLKS					
g996	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITLALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGNN NLKS					
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	190	200				
	DQIHANGKGYRKFAENLNQFLRKHGFRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAA	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAATATCAT	GAAACCGTGC	AGAAGGAAA	CATCCCGGCC	GTCCTCGTCG
401	CGGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATTT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTG	CGAGGAATAC	GGCATTCGCG	TGTTCCGGCG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAATATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTTG	CCGAAGATTT	GAATCAATTT
601	TTGAGAAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTELLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPALQK	LTGWNIVNGG	VSGDTSQAQL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLS DH
151	PLYEDLSEY	GIPLFGGAWA	EILGDN NLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					

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|||||
m996  MNRRTFLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGANPGESYPALQK
      10      20      30      40      50      60
a996.ppep  LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
m996  LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
a996.ppep  ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
m996  ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
a996.ppep  DQIHANGKGYRKFAEDLNQFLRKQGRFX
      190     200
m996  DQIHANGKGYRKFAEDLNQFLRKQGRFX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGCG TTGTCGCCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCCAGAC
251 CCCGTGCCCG CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTGT
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAT
501 GCAGTTTGGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CTTTGGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGTC CCGCCCGCTG ACCGGCATtG CCGACggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCCG cGTCAttagc GTTCCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSGLDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGAG CTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCCGATC
251 CCCGTGCCCG CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTGT
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CTTTGGGAAA

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1417

```
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CCGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCG TCCGCTTGGC GCGCCCGCTG ACCGCGCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGGT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCGCCGCGCG GACTTGTCTG GGTTCACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```
m997.pep
1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKS GSDYLLP KQDLGAI VAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQW LLCRGRGLP ENEVSAVISV SDRVGAFAFNR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSGVLT KKS GSDYLLPKQDLGAI VAE PALAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLT KKS GSDYLLPKQDLGAI VAE PALADLQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAA IATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFAFNR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRGL-GLPENEVSAVISVSDRVGAFAFNRADKAHAD					
	310	320	330	340	350	

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```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRVHAITTVYLRY
           |||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRVHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTQWLLCRGRLGLFENEVSAVISVSDRVGAFANRAWADKVHADL
           |||
m997      AEPVRLPAPLTGLADGTQWLLCRGRLGLFENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
           |||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTAAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTC CAGCTTAAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGA AAAAGAACCAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QOSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKTDGKY DLTLMVDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTIT DKLGESACK
151 QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGCGGTGT TGCGCCTGAT GAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCC GCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTGGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA ACAGCGGAAAC GTGCCGCGTG CCGCCGTAAT
651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGCGCA CCGCGCCCTA
801 CCACGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGCGTG ACCGGAAGTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAAGCT CGGACTGCCT GAAACGAAAG
1001 TGTCGCCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAACCCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACC CCGCCGCGG GATTGTGCTG GGTTCGACCG GCACCGCATC
1151 CAGCCGATGC CCCGCCCGG GATTGTGCTG GGTTCGACCG GCACCGCATC
1201 TTCCCGCGG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 GCGCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRIMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHLGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGPEPDA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVQW LLCRGLGLP ENEVSAVISV SDRVGAFAFR
351 AWADKVHADL KRILPHLGE EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAQDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVLRIMKTI GSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHLGGVLL					
m997	NGQHILLGAYRGVLRIMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHLGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPFAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWALNT					
m997	ARRAPFAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

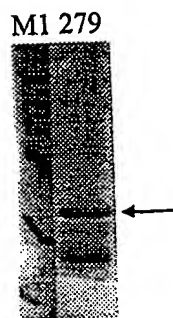
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

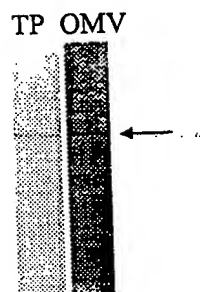
Fig. 2

279 (10.5 kDa)

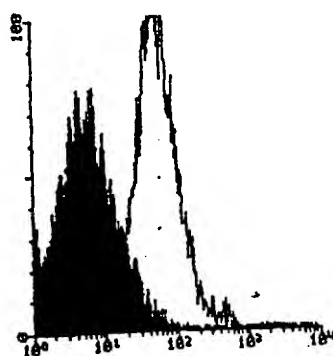
A) PURIFICATION



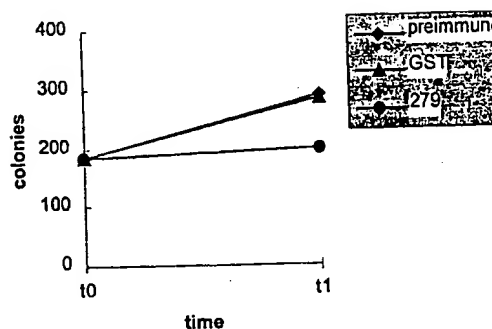
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

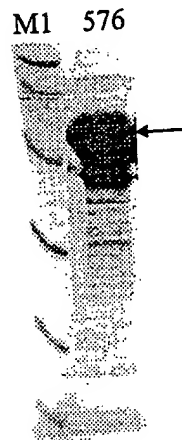
279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 3

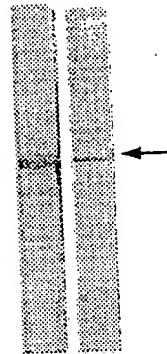
576 (27.8 kDa)

A) PURIFICATION

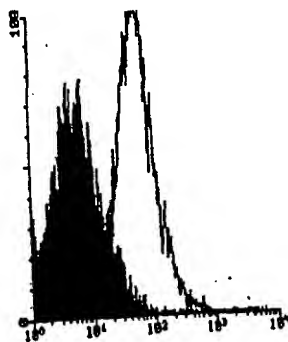


B) WESTERN BLOT

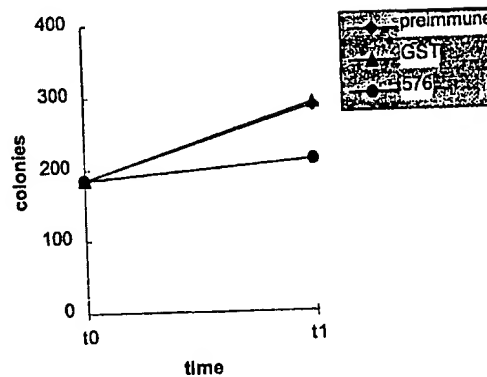
TP OMV



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay: positive

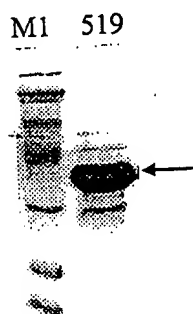
576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

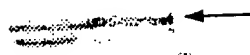
519 (33 kDa)

A) PURIFICATION

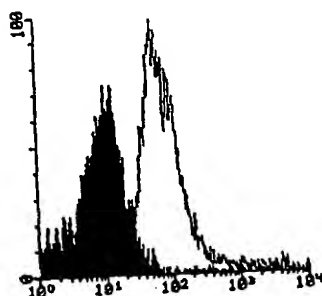


B) WESTERN BLOT

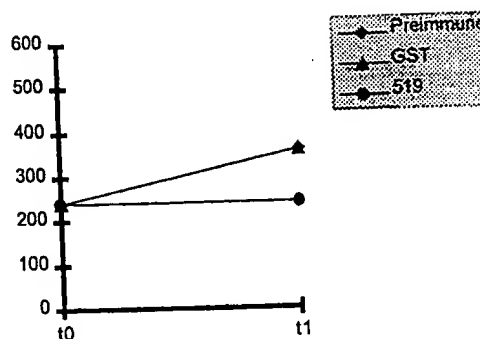
TP OMV



C) FACS

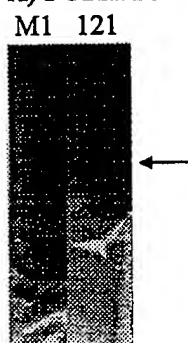
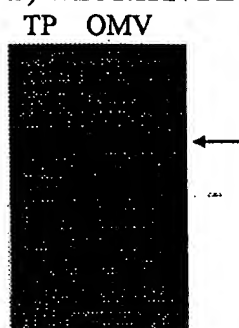
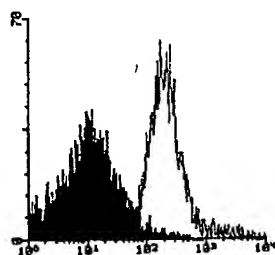
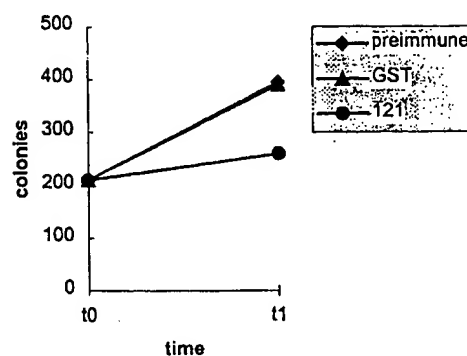


D) BACTERICIDAL ASSAY

E) ELISA assay: positive

519

The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

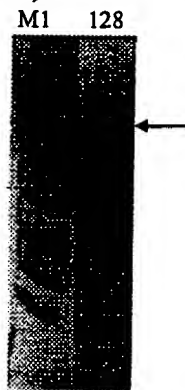
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

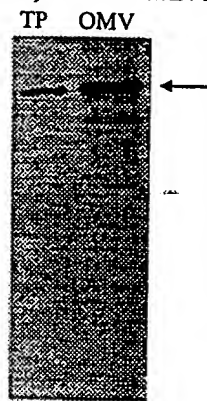
128 (101 kDa)

Fig. 6

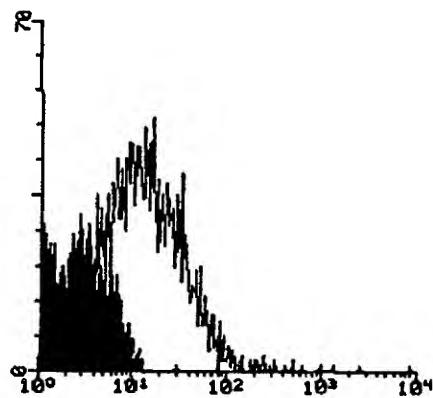
A) PURIFICATION



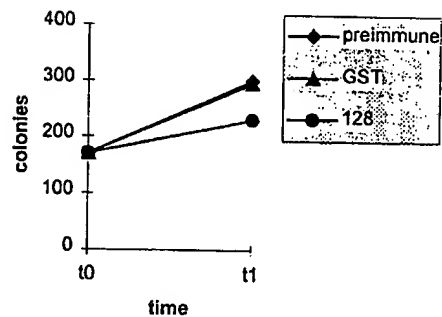
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



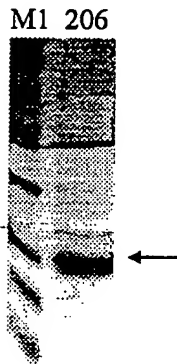
E) ELISA assay: positive

128

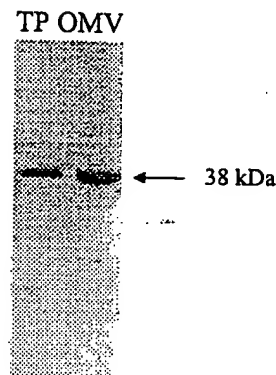
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

A) PURIFICATION



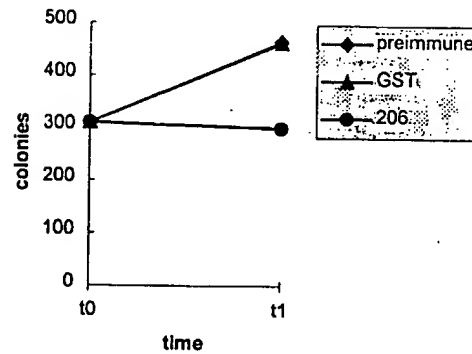
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

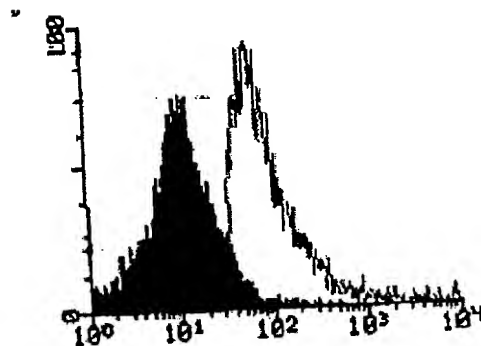
Fig. 8

287 (78 kDa)

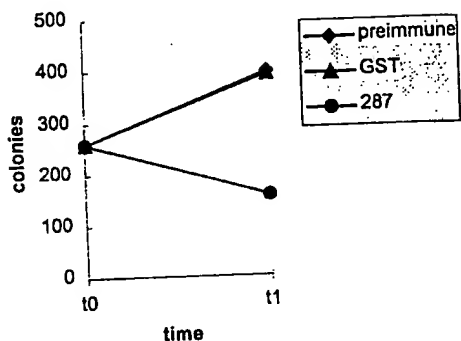
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY

D) ELISA assay : positive

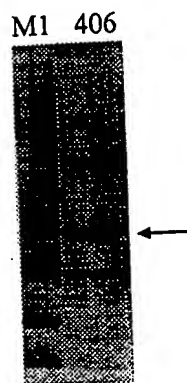
287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

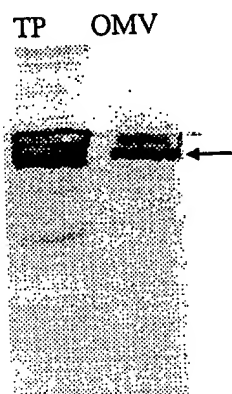
406 (33 kDa)

Fig. 9

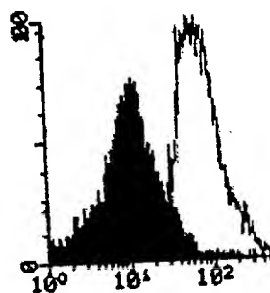
A) PURIFICATION



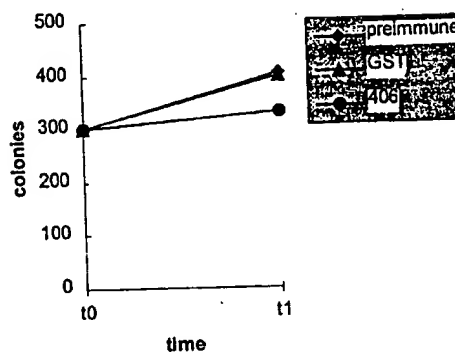
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY

E) ELISA assay : positive

406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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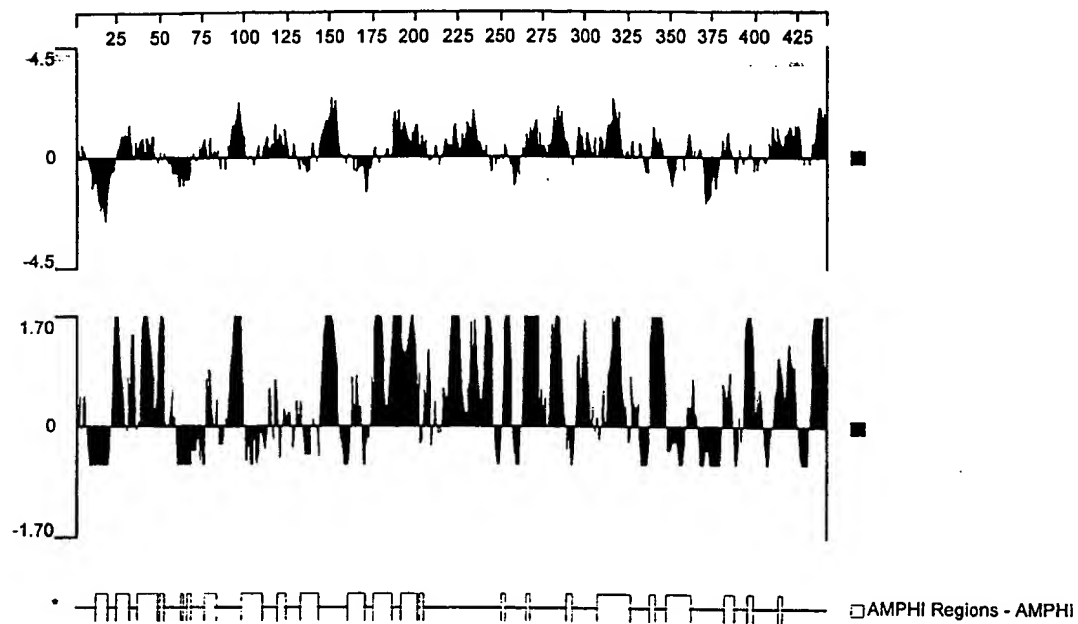
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

10/30

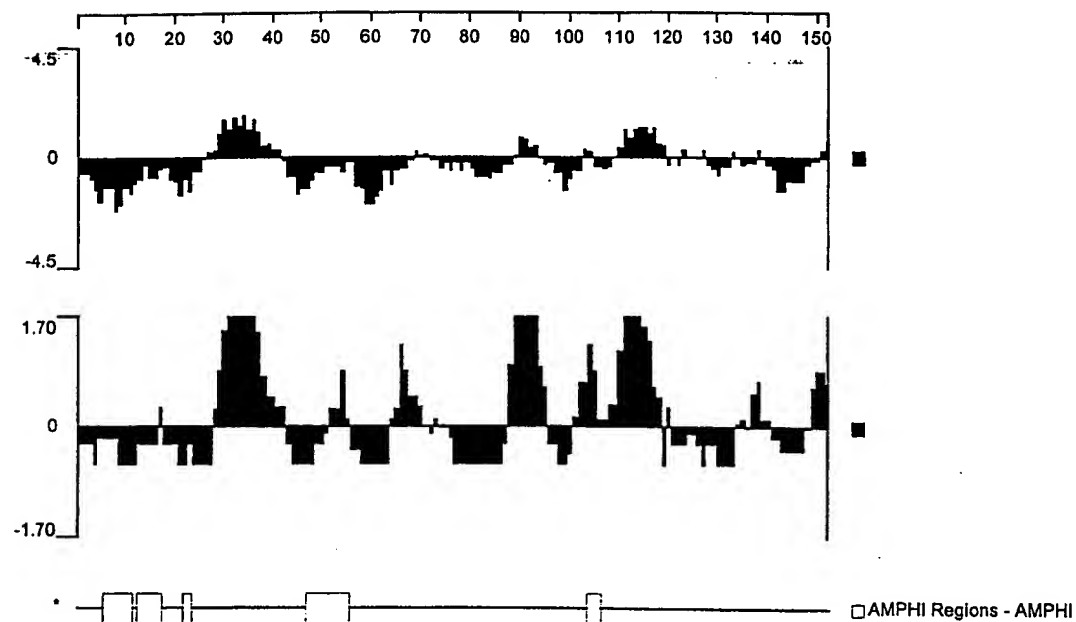
279Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

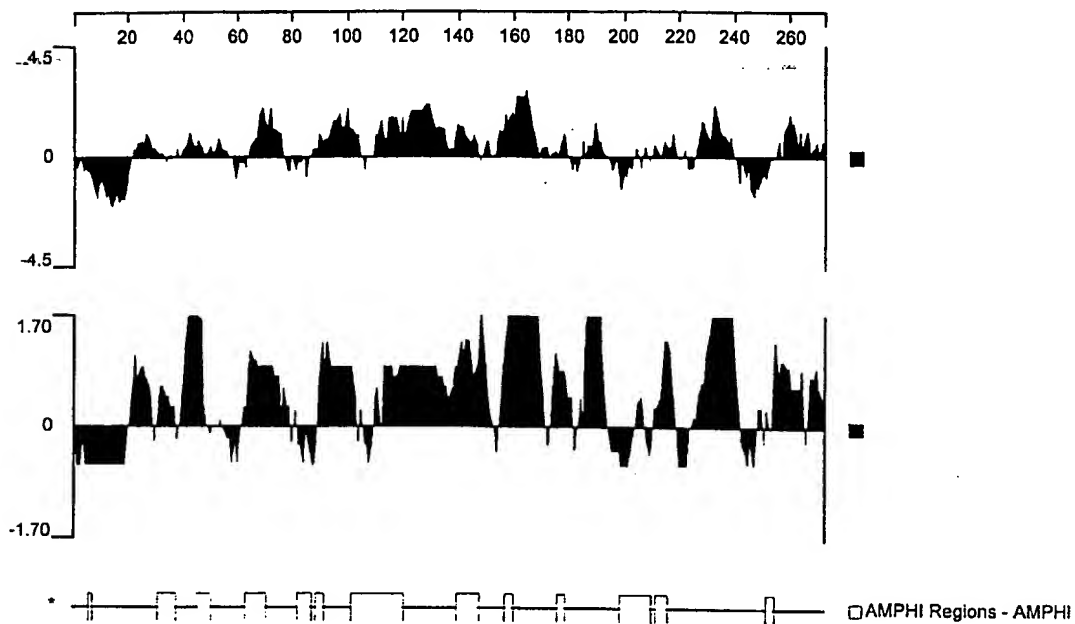
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

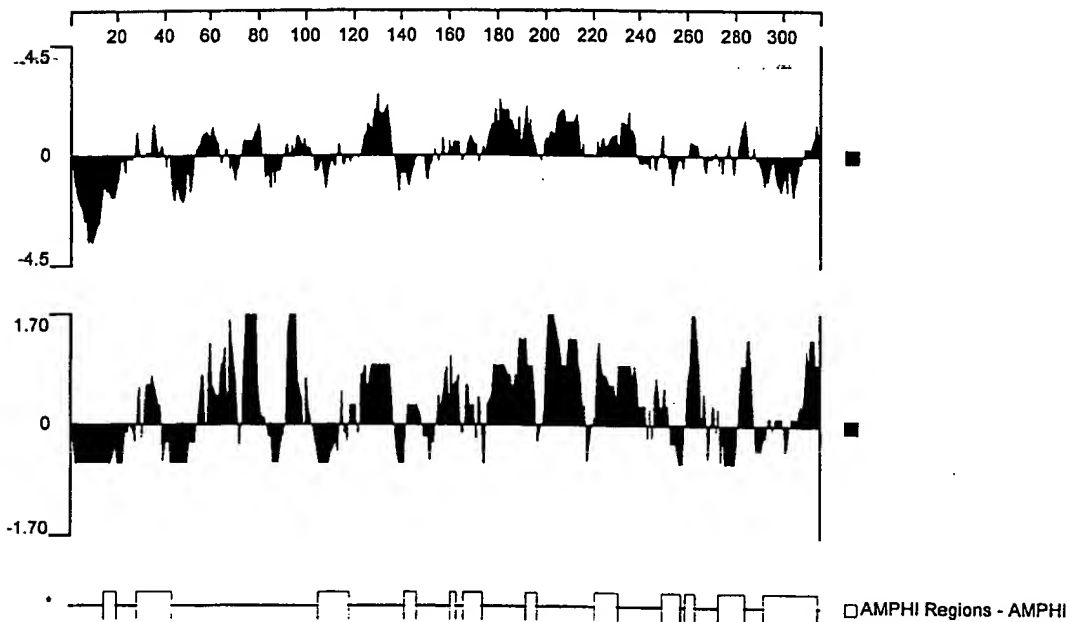
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

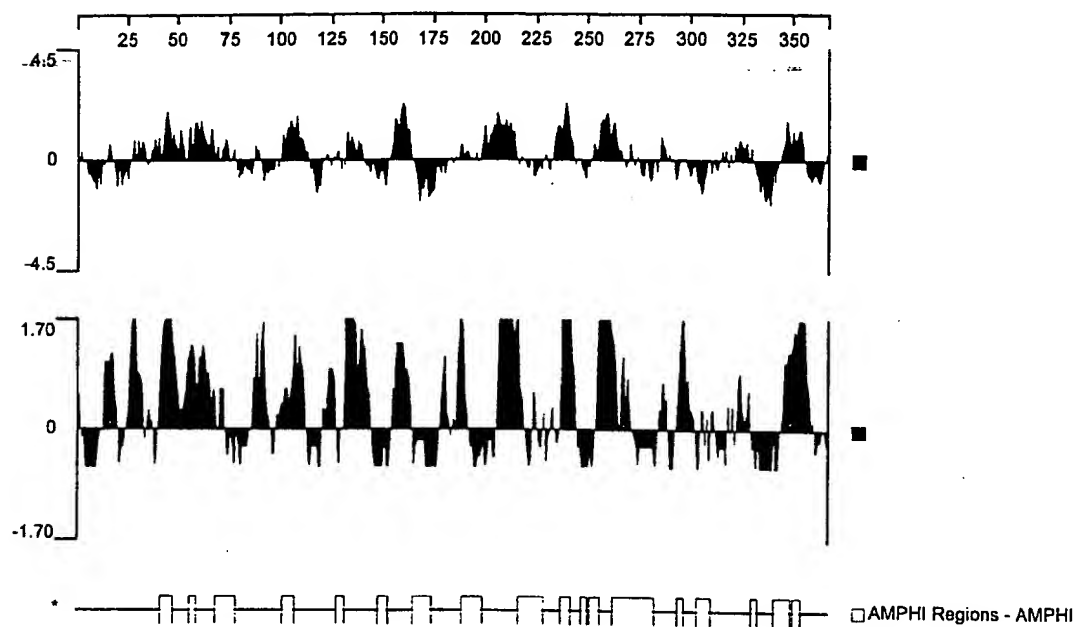
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

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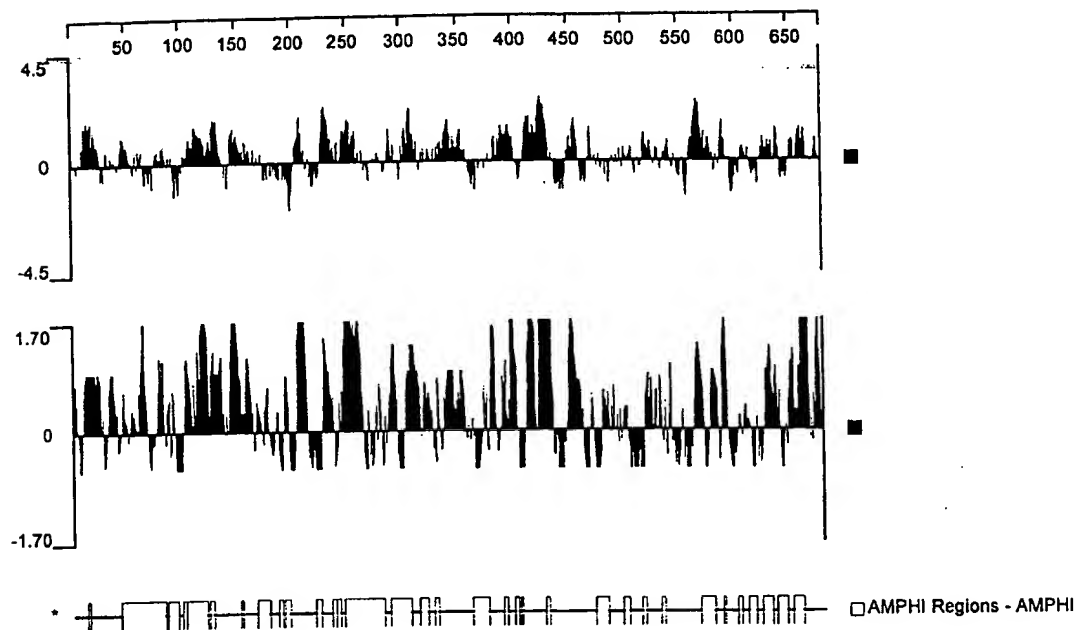
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

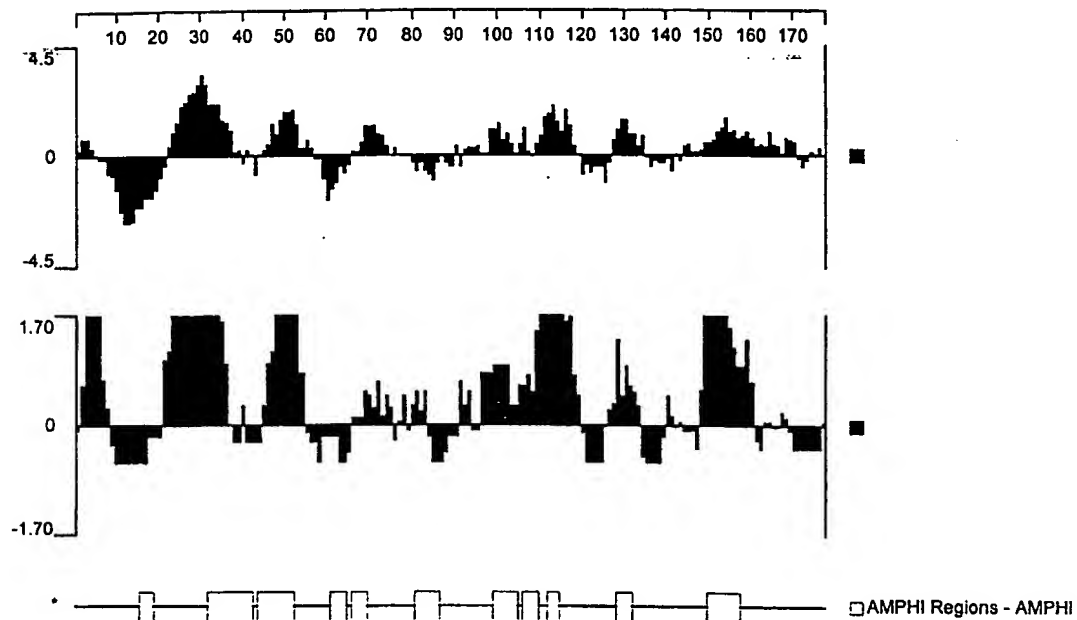
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

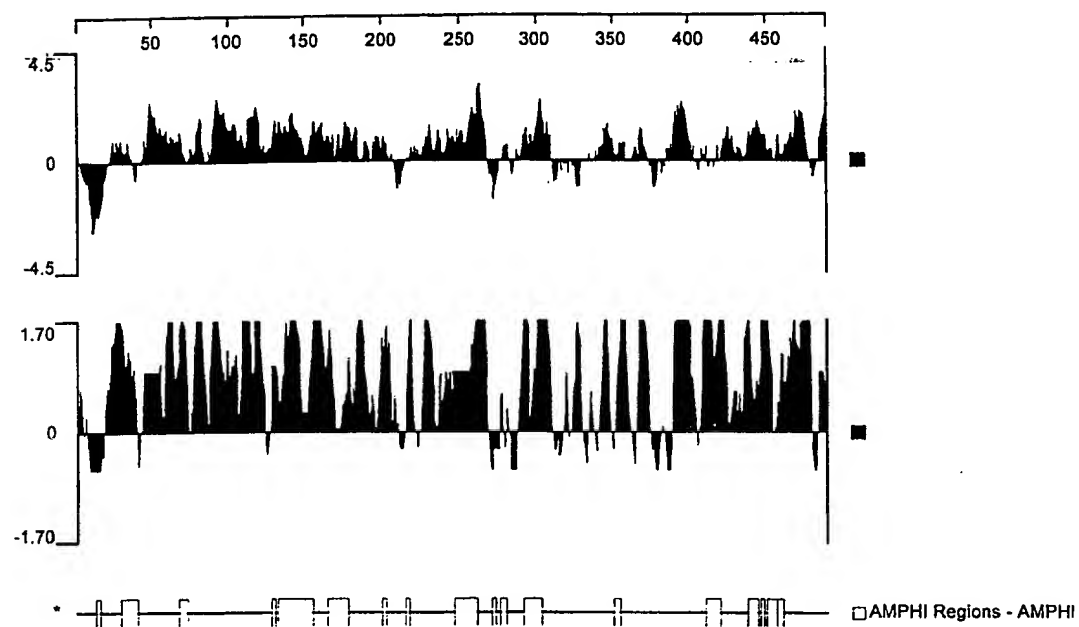
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

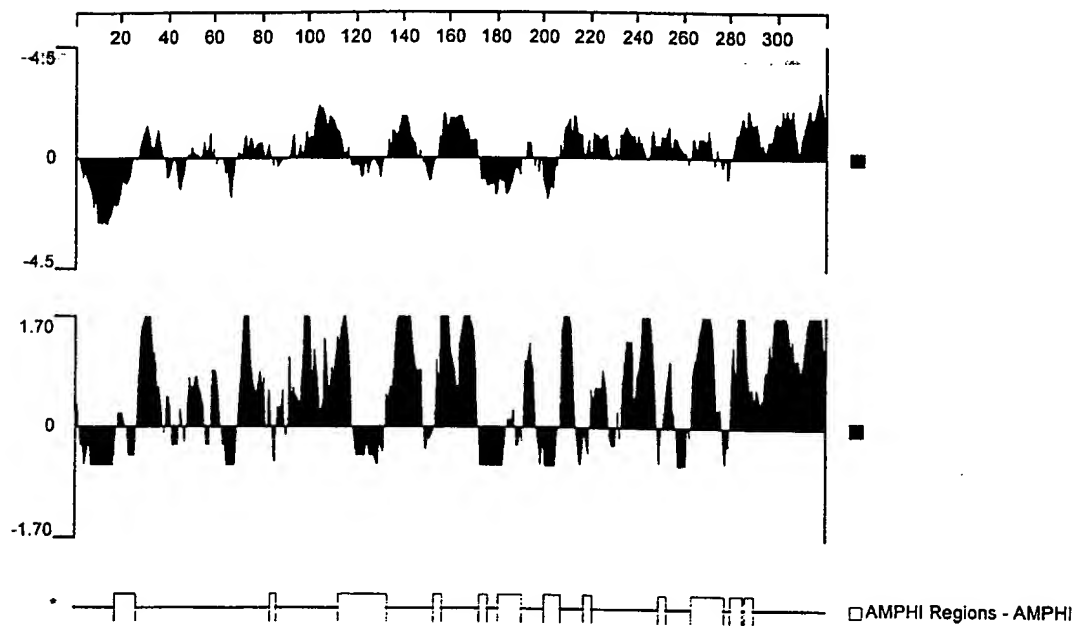
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

zo05_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo08_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
z2491	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo11_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo20_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo01_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo09_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo12_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo22_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo23_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo24_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo25_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo26_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo96_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo02_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
zo04_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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zo14_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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zo33_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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zo08_225	61	NADELIGSAMGLNE
z2491	61	NADELIGSAMGLNE
zo11_225	61	NADELIGSAMGLNE
zo20_225	61	NADELIGSAMGLNE
zo01_225	61	NADELIGSAMGLNE
zo09_225	61	NADELIGSAMGLNE
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zo15_225	61	NADELIGSAMGLNE
fa1090	61	NADELIGSAMGLNE
zo32_225	61	NADELIGSAMGLNE
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Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
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zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C


```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
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fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
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fa1090 117 .ESANTGNNQAPAGSDSAPASNPAPANGGSDFGRITNGNSVVIDGPSQNTLTHCKGDS

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287_2 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKKGKNDGKNDKFVGLVADSVQMKGINOYII
287_21 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKKGKNDGKNDKFVGLVADSVQMKGINOYII
z2491 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKKGKNDGKNDKFVGLVADSVQMKGINOYII
287_9 238 CORDFLDEEAPSKSEFEKLSDAKISNYKKKGKNDGKNDKFVGLVADSVQMKGINOYII
fa1090 176 CNGNDLDEEAPSKSEFEKLSDAKISNYKKKGKNDGKNDKFVGLVADSVQMKGINOYII

287_14 290 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_2 290 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_21 286 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
z2491 286 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_9 293 IYKQKSAS...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
fa1090 232 FYTDKPPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG

287_14 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_2 348 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA

287_14 408 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_2 408 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_21 404 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDFGSKSVDSGIIDSGDLHMGTOQKFKAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

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FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

z2491_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519 ^{ass}	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519 ^{ass}	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519 ^{ass}	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519 ^{ass}	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519 ^{ass}	121	RMELDKTFEERDEINSTVV	ALDEAAGAGWVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

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z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

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z2491_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
zv29_519ass 241 LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

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z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
zv12_519 301 ISAGMKIIDSSKTAK*
zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*

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Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

fa1090	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm33asbc	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm32asbc	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D